

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:34:32 ; Search time 1030.5 Seconds  
(without alignments)  
1241.095 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagccaccagtcgcaaa 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 2296392

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBdb1:\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sta:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_ncg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.8	74.0	20	2	CS142282 Sequence
C 2	14.8	74.0	23	2	AX555832 Sequence
C 3	14.2	71.0	25	2	BD137038 Method of
C 4	14.2	71.0	25	2	I49790 Sequence 13
C 5	13.8	69.0	41	2	BD210966 Polyvalen
C 6	13.8	69.0	41	2	AR235363 Sequence
C 7	13.6	68.0	39	2	CQ792409 Sequence
C 8	13.6	68.0	34	2	CQ792359 Sequence
C 9	13.2	66.0	20	2	CS142185 Sequence
C 10	13.2	66.0	22	2	AR279075 Sequence
C 11	13.2	66.0	27	5	AY082793 Homo sapi
C 12	13.2	66.0	36	6	MMPE5RNA
C 13	13.2	66.0	42	2	HSTRK3X2
C 14	13.2	66.0	48	5	AX555817 Sequence
C 15	13.2	66.0	50	2	HS305425 Homo sapi
C 16	13.2	66.0	50	2	CQ006932 Sequence
C 17	13.2	66.0	50	2	AR686596
C 18	13	65.0	43	2	DD176025 Methods f

19	13	65.0	43	2	DD176029	DD176029 Methods f
C 20	12.8	64.0	20	2	AR686610	AR686610 Sequence
C 21	12.8	64.0	32	2	BD097652	BD097652 A method
C 22	12.8	64.0	38	2	AR089797	AR089797 Sequence
C 23	12.8	64.0	50	2	CS196297	CS196297 Sequence
C 24	12.8	64.0	50	2	CS196298	CS196298 Sequence
C 25	12.8	64.0	50	2	AX199554	AX199554 Sequence
C 26	12.6	63.0	24	2	A14187	A14187 Sequence 2
C 27	12.6	63.0	33	2	AX327342	AX327342 Sequence
C 28	12.6	63.0	50	2	AR681179	AR681179 Sequence
C 29	12.6	63.0	50	2	AX160912	AX160912 Sequence
C 30	12.4	62.0	20	2	AR009483	AR009483 Sequence
C 31	12.4	62.0	20	2	AR064141	AR064141 Sequence
C 32	12.4	62.0	20	2	I35562	I35562 Sequence 9
C 33	12.4	62.0	20	2	AR437003	AR437003 Sequence
C 34	12.4	62.0	21	2	CQ880089	CQ880089 Sequence
C 35	12.4	62.0	23	2	AR009484	AR009484 Sequence
C 36	12.4	62.0	23	2	AR064142	AR064142 Sequence
C 37	12.4	62.0	23	2	I35563	I35563 Sequence 10
C 38	12.4	62.0	24	2	A13348	A13348 Primer DNA
C 39	12.4	62.0	24	7	BX545880	BX545880 Arabidops
C 40	12.4	62.0	25	2	BD139760	BD139760 Ion chann
C 41	12.4	62.0	25	2	CS245405	CS245405 Sequence
C 42	12.4	62.0	25	2	AR307666	AR307666 Sequence
C 43	12.4	62.0	25	2	AR483522	AR483522 Sequence
C 44	12.4	62.0	27	2	AX277398	AX277398 Sequence
C 45	12.4	62.0	27	7	BX545749	BX545749 Arabidops

#### ALIGNMENTS

RESULT 1  
LOCUS CS142282 Sequence 243 from Patent WO2005071080. 20 bp DNA linear PAT 17-AUG-2005  
DEFINITION CS142282  
ACCESSION CS142282  
VERSION CS142282.1 GI:73532182

#### KEYWORDS

SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

#### REFERENCE

1  
AUTHORS Bhanot, S.  
TITLE Modulation of glucocorticoid receptor expression  
JOURNAL Patent: WO 2005071080-A 243 (04-AUG-2005;  
ISIS PHARMACEUTICALS, INC. (US)  
FEATURES Location/Qualifiers

#### ORIGIN

1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Antisense Compound"

Query Match 74.0%; Score 14.8; DB 2; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.5e+05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGCCACCAAGTCCAA 20  
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DB 19 TGAACCAACGAGCCCAA 2

RESULT 2  
AX555832 43 bp DNA linear PAT 27-NOV-2002  
LOCUS AX555832 Sequence 428 from Patent WO2070755.  
DEFINITION AX555832  
ACCESSION AX555832  
VERSION AX555832.1 GI:25899304

KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct

other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Lyamichev, V. I., Kaiser, M. W. and Lyamicheva, N.  
TITLE Pen endonucleases  
JOURNAL Patent: WO 02070755-A 428 12-SEP-2002;  
Third Wave Technologies, Inc. (US)  
FEATURES Location/Qualifiers

source 1..43  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

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Query Match 74.0%; Score 14.8; DB 2; Length 43;  
Best Local Similarity 88.9%; Pred. No. 1.3e+05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGCCACCAAGTGTCCA 20  
DB 32 TGAGCCACCAAGTGTCCA 15

RESULT 3  
BD137038 25 bp DNA linear PAT 18-SEP-2002  
LOCUS Method of determining nucleotide sequence and protein encoded by  
DEFINITION transfection into host.  
ACCESSION BD137038  
VERSION BD137038.1 GI:23231983  
KEYWORDS JP 2002508957-A/17.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.

REFERENCE 1 (bases 1 to 25)  
AUTHORS Clappe, G.D., Erwin, R.L., Fitzmaurice, W.P., Hanley, K.M.,  
Kumagai, M.H., Lindbo, J.A., McGee, D.R., Padgett, H.S. and Pogu, G.P.  
TITLE Method of determining nucleotide sequence and protein encoded by  
JOURNAL transfection into host  
PATENT: JP 2002508957-A 17 26-MAR-2002;  
LARGE SCALE BIOLOGY CORP

COMMENT OS Virus  
PN JP 2002508957-A/17  
PD 26-MAR-2002  
PF 15-JAN-1999 JP 2000540219  
PR 16-JAN-1998 US 09/008186  
PI GUY DELLA CIOPIA, ROBERT L ERWIN, WAYNE P  
FITZMAURICE, KATHLEEN M

PI HANLEY,  
PI MONTTO H KUMAGAI, JOHN A LINDBO, DAVID R MCGEE, HAL S PADGETT, PI  
GREGORY P POGUE  
PC C12N15/09, C12N15/00, C12Q1/68//A01H1/00, C12N5/10, C12N15/00, PC  
C12N15/00,  
PC C12N5/00  
CC Method of determining nucleotide sequence and protein encoded  
CC by  
CC transfection into host.  
FH Key Location/Qualifiers  
FT source 1..25  
/organism="Virus".

FEATURES source 1..25  
Location/Qualifiers  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

## ORIGIN

Query Match 71.0%; Score 14.2; DB 2; Length 25;  
Best Local Similarity 84.2%; Pred. No. 2.8e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGAGCCACCAAGTGTCCA 20  
DB 19 ATGAGCCACCAAGTGTCCA 1

RESULT 4  
LOCUS 149790 25 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 13 from patent US 5641661.  
ACCESSION 149790  
VERSION 149790.1 GI:2472010  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
unclassified.

REFERENCE 1 (bases 1 to 25)  
AUTHORS Kumagai, M.H. and Sverlow, G.G.  
TITLE Pichia pastoris alcohol oxidase ZZA1 and ZZA2 regulatory regions  
JOURNAL for heterologous gene expression  
PATENT: US 5641661-A 13 24-JUN-1997;  
FEATURES Location/Qualifiers

source 1..25  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Query Match 71.0%; Score 14.2; DB 2; Length 25;  
Best Local Similarity 84.2%; Pred. No. 2.8e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGAGCCACCAAGTGTCCA 20  
DB 19 ATGAGCCACCAAGTGTCCA 1

RESULT 5  
BD210966 41 bp DNA linear PAT 17-JUL-2003  
LOCUS Polyvalent unsaturated fatty acid in plant.  
DEFINITION BD210966  
ACCESSION BD210966.1 GI:33020736  
VERSION JP 2002517255-A/1.  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
unclassified sequences.

REFERENCE 1 (bases 1 to 41)  
AUTHORS Knutson, D.  
TITLE Polyvalent unsaturated fatty acid in plant  
JOURNAL Patent: JP 2002517255-A 1 18-JUN-2002;  
CALGENE LLC

COMMENT OS Artificial Sequence  
PN JP 2002517255-A/1  
PD 18-JUN-2002  
PF 10-JUN-1999 JP 2000553604  
PR 12-JUN-1998 US 60/089043  
PI DEBBIE KNUTSON  
PC C12N15/09, A01H5/00, C12P7/64, C12N15/00  
CC Synthetic oligonucleotide  
FH Key Location/Qualifiers  
FT source 1..41  
/organism="Artificial Sequence".

FEATURES source 1..41  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

## ORIGIN

Query Match 69.0%; Score 13.8; DB 2; Length 41;  
Best Local Similarity 88.2%; Pred. No. 3.9e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCT 17  
DB 34 AATGAGCCACCAAGTGTCT 18

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RESULT 6
REFERENCE AR235363/c 41 bp DNA linear PAT 20-DEC-2002
AUTHORS AR235363
TITLE Sequence 3 from patent US 6459018.
JOURNAL AR235363
DEFINITION AR235363
ACCESSION AR235363
VERSION AR235363.1 GI:27278499
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 41)
TITLE Knutzen,D.
JOURNAL Polyunsaturated fatty acids in plants
DEFINITION Patent: US 6459018-A 3 01-OCT-2002;
ACCESSION Monsanto Technology LLC; St. Louis, MO
VERSION
KEYWORDS
FEATURES
SOURCE 1..41
/molecule="synthetic construct"
/db_xref="taxon:32630"
/notes="Description of Artificial Sequence: PCR Primer"
ORIGIN
Query Match 69.0%; Score 13.8; DB 2; Length 41;
Best Local Similarity 88.2%; Pred. No. 3.9e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AATGAGCCACGAGTTC 17
Db 34 AATGAGCCACGAGTTC 18

RESULT 7
LOCUS CQ792409 29 bp DNA linear PAT 29-MAR-2004
DEFINITION Sequence 154 from Patent WO2004020642.
ACCESSION CQ792409
VERSION CQ792409.1 GI:45823909
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS McCourt,P., Ghassemi,M., Cutler,S. and Bonetta,D.
TITLE Stress tolerance and delayed senescence in plants
JOURNAL Patent: WO 2004020642-A 154 11-MAR-2004;
Performance Plants, Inc. (CA)
FEATURES
SOURCE 1..29
/location/Qualifiers
/molecule="synthetic construct"
/db_xref="taxon:32630"
/notes="Description of Artificial Sequence: PCR Primer"
ORIGIN
Query Match 68.0%; Score 13.6; DB 2; Length 29;
Best Local Similarity 80.0%; Pred. No. 5.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 AATGAGCCACGAGTTC 20
Db 1 AAAGAGCTCCAGTTC 20

RESULT 8
LOCUS CQ792359 34 bp DNA linear PAT 29-MAR-2004
DEFINITION Sequence 104 from Patent WO2004020642.
ACCESSION CQ792359
VERSION CQ792359.1 GI:45823868
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
ORIGIN
Query Match 66.0%; Score 13.2; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 8.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 TGAAGCCACGAGTTC 20
Db 19 TAAAGCCACGAGTTC 2

RESULT 9
LOCUS CS142185 20 bp DNA linear PAT 17-AUG-2005
DEFINITION Sequence 146 from Patent WO2005071080.
ACCESSION CS142185
VERSION CS142185.1 GI:73532085
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS Bhanot,S.
TITLE Modulation of glucocorticoid receptor expression
JOURNAL Patent: WO 2005071080-A 146 04-AUG-2005;
ISIS PHARMACEUTICALS, INC. (US)
FEATURES
SOURCE 1..20
/location/Qualifiers
/molecule="synthetic construct"
/db_xref="taxon:32630"
/notes="Antisense Compound"
ORIGIN
Query Match 66.0%; Score 13.2; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 8.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 TGAAGCCACGAGTTC 20
Db 19 TAAAGCCACGAGTTC 2

RESULT 10
LOCUS AR279075 22 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 208 from patent US 6514694.
ACCESSION AR279075
VERSION AR279075.1 GI:29713718
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 22)
TITLE Milhausen,M.J.
JOURNAL Methods for the detection of encypted parasites
DEFINITION Patent: US 6514694-A 208 04-FEB-2003;
ACCESSION Hesk Corporation; Fort Collins, CO
VERSION
KEYWORDS
FEATURES
SOURCE 1..22
/location/Qualifiers
/molecule="synthetic construct"
/db_xref="taxon:32630"
/notes="Antisense Compound"
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ORIGIN

Query Match 66.0%; Score 13.2; DB 2; Length 22;  
 Best Local Similarity 83.3%; Pred. No. 8.4e+05;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGAGCCAGCAGTGTCCA 19  
 |||||  
 21 ATGATGCACGAGTGTCCA 4

RESULT 11  
 AY082793 27 bp DNA linear PRI 08-APR-2003  
 LOCUS AY082793  
 DEFINITION Homo sapiens clone 101.18 T cell receptor beta chain gene, partial cds.  
 ACCESSION AY082793 GI:29647040  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 27)  
 2 (bases 1 to 27)  
 Lin, W.L., Flincke, J.E., Sharer, L.R., Platsoucas, C.D. and Oleszak, E.L.  
 Oligoclonal T cells are infiltrating the brain of children with AIDS: sequence analysis revealed high proportions of identical beta-chain T-cell receptor (TCR) transcripts  
 Unpublished  
 JOURNAL  
 REFERENCE  
 AUTHORS Lin, W.L., Flincke, J.E., Sharer, L.R., Platsoucas, C.D. and Oleszak, E.L.  
 Direct Submission  
 Submitted (07-MAR-2002) Microbiology/Immunology, Temple University School of Medicine, 3400 North Broad Street, Philadelphia, PA 19140, USA

FEATURES  
 source  
 Location/Qualifiers  
 1..27  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="101.18"  
 /note="normal donor PBMC"  
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 /product="T cell receptor beta chain"  
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 /note="TCR beta; CDR3 region; contains Vbeta 2.1 Dbeta2.1  
 Vbeta2.5"  
 /codon\_start=1  
 /product="T cell receptor beta chain"  
 /protein\_id="AA03440.1"  
 /db\_xref="GI:29647041"  
 /translation="CASSDQETQ"

ORIGIN

Query Match 66.0%; Score 13.2; DB 5; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 8.1e+05;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGAGCCACGAGTGTCCA 20  
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 1 TGTGCCAGCAGTGTCCA 18

RESULT 12  
 MPM5RNA 36 bp mRNA linear ROD 07-FEB-1992  
 LOCUS MPM5RNA  
 DEFINITION M.musculus rearranged mRNA for T cell receptor beta chain  
 Vbeta13/Jbeta2.7 join.  
 X60865  
 VERSION X60865.1 GI:53624

KEYWORDS  
 SOURCE T-cell receptor beta chain; Vbeta13/Jbeta2.7 join.  
 ORGANISM Mus musculus (house mouse)  
 Mus musculus  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.  
 1 (bases 1 to 36)  
 Casanova, J.L., Romero, P., Widmann, C., Kourilsky, P. and Maryanski, J.L.  
 T cell receptor genes in a series of class I major histocompatibility complex-restricted cytotoxic T lymphocyte clones specific for a Plasmodium berghei nonapeptide: implications for T cell allelic exclusion and antigen-specific repertoire  
 J. Exp. Med. 174 (6), 1371-1383 (1991)

JOURNAL  
 PUBLISHED 1836010  
 2 (bases 1 to 36)  
 Casanova, J.L.  
 Direct Submission  
 Submitted (08-JUL-1991) J.L. Casanova, Ludwig Inst for Cancer Research, Lausanne Branch, Spallinger 1066, SWITZERLAND  
 H-2Kd-restricted CTL clone specific for a Plasmodium berghei circumsporozoite nonapeptide.  
 Location/Qualifiers  
 1..36  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="BALB/c; F1 (BALB/c x C57BL6)"  
 /db\_xref="taxon:10090"  
 /clone="PE5.1.1"  
 /haplotype="H-2d/Vbeta13"  
 /cell\_type="CTL clone"  
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 /codon\_start=1  
 /product="T cell receptor beta chain"  
 /protein\_id="CAA43255.1"  
 /db\_xref="GI:53625"  
 /translation="CASSFQYQYFG"

CDS  
 misc\_feature  
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 /note="Framework branch: FW1"  
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 /note="Vbeta13/Jbeta2.7 junction"  
 28..36  
 /note="Framework branch: FW2"

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 36;  
 Best Local Similarity 83.3%; Pred. No. 7.6e+05;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGAGCCACGAGTGTCCA 20  
 |||||  
 1 TGTGCCAGCAGTGTCCA 18

RESULT 13  
 HSTRK3X32 39 bp mRNA linear PRI 05-FEB-1997  
 LOCUS HSTRK3X32  
 DEFINITION H.sapiens mRNA for T cell receptor beta chain junctional region (clone K3-32).  
 269494  
 269494.1 GI:1770615  
 ACCESSION  
 KEYWORDS diversity region; joining region; T cell receptor; variable region.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 39)  
 Naserke, H.R., Durinovic-Bello, I., Seidel, D. and Ziegler, A.G.  
 The T-cell receptor beta chain CDR3 region of BV8S1/BJ155 transcripts in type 1 diabetes  
 Immunogenetics 45 (2), 87-96 (1996)



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REFERENCE      2 (bases 1 to 39)
AUTHORS        Naserke,H.E.
TITLE          Direct Submission
JOURNAL        Submitted (02-FEB-1996) Naserke H.E., Diabetes Research Institute,
                Koelner Platz 1, D-80804 Muenchen, FRG
FEATURES
SOURCE
1..39
/organism="Homo sapiens"
/mol_type="mRNA"
/isolate="type 1 diabetic patient FS"
/db_xref="taxon:9606"
/clone="K3-32"
/cell_type="lymphocytes"
/tissue_type="peripheral blood"
/note="HLA type: HLA-A31, 1; Cw3, 3; B62, 55; DRB1*1301,
0401; DRB3*0202, -; DQA1*0103, 0301; DQB1*0603, 0302;
DPB1*-; 01; DPB1*0301, 0201"
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/gene="V beta 8.1"
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13..17
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/gene="J beta 1.5"

ORIGIN
Query Match      66.0%; Score 13.2; DB 5; Length 39;
Best Local Similarity 83.3%; Pred. No. 7.5e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 TGAGCCACGAGTGCCAA 20
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Db      1 TGTGCCACGAGTCCCA 18

RESULT 14
AX555817/c      42 bp      DNA      linear      PAT 27-NOV-2002
LOCUS           Sequence 413 from Patent WO02070755.
DEFINITION      AX555817
ACCESSION       AX555817
VERSION         AX555817.1 GI:25899291
KEYWORDS
SOURCE
ORGANISM        synthetic construct
                other sequences; artificial sequences.
REFERENCE
1 Lyamichnev,V.I., Kaiser,M.W. and Lyamichnev,N.
  Pen endonucleases
  Patent: WO 02070755-A 413 12-SEP-2002;
  Third Wave Technologies Inc. (US)
  Location/Qualifiers
1..42
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match      66.0%; Score 13.2; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 7.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 TGAGCCACGAGTGCCAA 20
        |||||
Db      31 TGAGCCACGAGTCCAA 14

RESULT 15

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HSA305425
LOCUS           48 bp      DNA      linear      PRI 18-MAY-2001
DEFINITION      Homo sapiens partial TCRBV15J2S2 gene for T-cell receptor beta
                chain, junctional region, patient I CA, clone #18.
ACCESSION       AJ305425
VERSION         AJ305425.1 GI:11323060
KEYWORDS        junctional region; T-cell receptor beta chain; TCR beta chain;
                TCRBV15J2S2 gene; variable region.
SOURCE
ORGANISM        Homo sapiens (human)
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homiidae; Homo.
REFERENCE
1 Duchmann,R., Lambert,C., May,E., Hohlner,T. and Marker-Hermann,E.
  CD4+ and CD8+ clonal T cell expansions indicate a role of antigens
  in ankylosing spondylitis; a study in HLA-B27+ monozygotic twins
  Clin. Exp. Immunol. 123 (2), 315-322 (2001)
11207664
PUBMED
REFERENCE
AUTHORS        May,E.
TITLE          Direct Submission
JOURNAL        Submitted (18-NOV-2000) May E., Internal Medicine/Rheumatology,
                University of Texas Southwestern Medical Center at Dallas, 5323
                Harry Hines Blvd, Dallas, TX 75390-8884, USA
FEATURES
SOURCE
1..48
/organism="Homo sapiens"
/mol_type="genomic DNA"
/isolate="patient I CA"
/db_xref="taxon:9606"
/clone="#18"
/tissue_type="peripheral blood"
1..48
/gene="TCRBV15J2S2"
<1..>48
/gene="TCRBV15J2S2"
1..48
/gene="TCRBV15J2S2"
/note="N-D-N joining region (CDR3)"
/codon_start=1
/product="T-cell receptor beta chain"
/protein_id="CAC16912.1"
/db_xref="GI:11323061"
/translation="CATSDLGSGTGERLFRG"

ORIGIN
Query Match      66.0%; Score 13.2; DB 5; Length 48;
Best Local Similarity 83.3%; Pred. No. 7.2e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 TGAGCCACGAGTGCCAA 20
        |||||
Db      1 TGTGCCACGAGTCCCTA 18

Search completed: May 21, 2006, 22:09:05
Job time : 1033.5 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using SW model

Run on: May 21, 2006, 21:34:08 / Search time 386 Seconds  
(without alignments)  
361.256 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagccaccagtcgca 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 5244920 seqs, 348612431 residues

Total number of hits satisfying chosen parameters: 5218826

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_8:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001s:\*

5: geneseqn2001b:\*

6: geneseqn2002a:\*

7: geneseqn2002b:\*

8: geneseqn2003a:\*

9: geneseqn2003b:\*

10: geneseqn2003c:\*

11: geneseqn2003d:\*

12: geneseqn2004a:\*

13: geneseqn2004b:\*

14: geneseqn2005a:\*

15: geneseqn2006a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	13	ADQ88722 Human HIF
2	20	100.0	20	13	ADQ88721 Human HIF
3	18.4	92.0	20	13	AAK78996 Human HIF-1alpha
4	18	90.0	20	13	ADT78617 HIF1alpha
5	17.4	87.0	19	14	ADZ58028 Sense sIR
6	17.4	87.0	19	14	ADZ58248 Antisense
7	16.4	82.0	32	10	ABZ83188 Toxicology
8	14.8	74.0	20	14	ABZ86823
9	14.8	74.0	20	15	ABZ86823
10	14.8	74.0	20	15	ABZ86823
11	14.2	71.0	21	14	ADZ53245 FEN-1 rel
12	14.2	71.0	25	2	AAZ80533
13	14.2	71.0	25	2	AAZ80533
14	14	70.0	20	10	ACZ58076 Human PRD
15	14	70.0	24	2	ADZ77414 Canine di
16	13.8	69.0	41	3	AAZ59866 C. elegans
17	13.8	69.0	41	3	AAZ5381 Omega-3-d
18	13.6	68.0	29	10	ADK41210 BnCP

19	13.6	68.0	29	12	ADM98488	Adm98488 Plant tra
20	13.6	68.0	29	15	AEF71319	Aef71319 BnCP-HP-
21	13.6	68.0	29	15	AEF9792	Aef9792 CaCP pren
22	13.6	68.0	34	10	ADK41180	Adk41180 AtCP Caa
23	13.6	68.0	34	12	ADM98452	Adm98452 Plant tra
24	13.6	68.0	34	15	AEF71270	Aef71270 AtCP-HP-
25	13.6	68.0	34	15	AEF9742	Aef9742 CaCP pren
26	13.4	67.0	20	11	AEZ9517	Aez9517 SNF conta
27	13.2	66.0	20	5	ABZ5611	Abz5611 Antisense
28	13.2	66.0	20	12	ADH63395	Adh63395 Human glt
29	13.2	66.0	20	12	ADH64247	Adh64247 Human glt
30	13.2	66.0	20	12	ADH63882	Adh63882 Human glt
31	13.2	66.0	20	14	AEZ8526	Aez8526 Human glt
32	13.2	66.0	20	15	AEF79537	Aef79537 Human glt
33	13.2	66.0	21	14	ACL45856	ACL45856 CDH6 targ
34	13.2	66.0	21	14	ACL45526	ACL45526 CDH6 targ
35	13.2	66.0	21	14	ACL45857	ACL45857 CDH6 sIRN
36	13.2	66.0	21	14	ACL45858	ACL45858 CDH6 sIRN
37	13.2	66.0	22	2	AAZ91339	Aaz91339 Primer fo
38	13.2	66.0	22	4	AAZ42662	Aaz42662 T. gondii
39	13.2	66.0	22	10	ADG17258	Adg17258 T. gondii
40	13.2	66.0	25	9	ACK30818	ACK30818 Human mtc
41	13.2	66.0	42	6	ADZ53230	Adz53230 FEN-1 rel
42	13.2	66.0	50	4	AAZ32364	Aaz32364 Human SNP
43	13.2	66.0	50	6	ABZ06034	Abz06034 Human leu
44	13.2	66.0	50	12	ADP12724	Adp12724 50-met ol
45	13.2	65.0	22	11	ADM47308	Adm47308 NOVA olig

## ALIGNMENTS

RESULT 1	ADQ88722	standard; DNA; 20 BP.
ID	ADQ88722	
XX	ADQ88722:	
AC	ADQ88722:	
XX	ADQ88722:	
DT	21-OCT-2004	(first entry)
XX	ADQ88722:	
XX	ADQ88722:	
DE	Human HIF-1 antisense oligonucleotide RX-0047.	
XX	ADQ88722:	
KW	RX-0047: RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;	
KW	cancer; infection; inflammation; tumour formation; ss;	
KW	antisense oligonucleotide; antisense technology.	
XX	ADQ88722:	
OS	Homo sapiens.	
XX	ADQ88722:	
PN	US2004152655-A1.	
XX	ADQ88722:	
XX	ADQ88722:	
PD	05-AUG-2004.	
PF	28-JAN-2004; 2004US-00766185.	
XX	ADQ88722:	
PR	31-JAN-2003; 2003US-0444367P.	
XX	ADQ88722:	
XX	ADQ88722:	
PA	(YOON/) YOON H.	
PA	(MAOL/) MAO L.	
PA	(LEEF/) LEE Y B.	
PA	(AHNC/) AHN C.	
PA	(JIAN/) JIANG X.	
XX	ADQ88722:	
PI	Yoon H, Mao L, Lee YB, Ahn C, JIANG X,	
XX	ADQ88722:	
DR	WPI; 2004-561492/54.	
XX	ADQ88722:	
PT	New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a	
PT	nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),	
PT	useful for inhibiting expression of HIF-1 and inducing cytotoxicity in	
XX	several cancer cells.	
XX	ADQ88722:	
PS	Claim 1; SEQ ID NO 2; 35pp; English.	



DB 8 AGTGAGCCACGAGTCCAA 27

RESULT 4  
ADT78617  
ID ADT78617 standard; DNA; 20 BP.

XX  
AC ADT78617/  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE H191alpha cDNA, antisense oligonucleotide ISIS #298743.  
XX  
KM Antisense therapy; human; hypoxia-inducible factor 1 alpha;  
KM hypoxia-inducible factor 2 alpha; H191alpha; HIF2alpha;  
KM hyperproliferative disorder; cancer; p53; angiogenic disorder;  
KM eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;  
KM psoriasis; atherosclerosis; smooth muscle cell proliferation;  
KM blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;  
KM ophthalmological; antiinflammatory; respiratory; vasotropic; mouse; rat;  
KM phosphorothioate; ss.  
XX  
OS Homo sapiens.  
OS Mus musculus.  
OS Rattus sp.

XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone. All cytidines are 5-methylcytidines"  
FT modified\_base 1..5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-Methoxyethyl (2'-MOE) nucleotides"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-Methoxyethyl (2'-MOE) nucleotides"  
XX  
PN US2004220393-A1.  
XX  
PD 04-NOV-2004.  
XX  
PF 21-NOV-2003; 2003US-00719370.  
XX  
PR 23-NOV-2002; 2002US-00304126.  
XX  
PA (WARD/) WARD D T.  
PA (DOBI/) DOBI K W.  
PA (MARCU/) MARCUSON E G.  
PA (FREIER/) FREIER S W.  
XX  
PI Ward DT, Doble KW, Marcuson EG, Freier SM;  
XX  
DR WPI; 2004-774955/76.  
XX  
PT New antisense compound which inhibits the expression of hypoxia-inducible factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating hyperproliferative disorder, e.g. cancer carrying a p53 mutation.  
XX  
PS Claim 27; SEQ ID NO 187; 195pp; English.

XX  
CC The present invention relates to antisense compounds targeted to nucleic acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound comprises an antisense oligonucleotide that specifically hybridises with the nucleic acid and inhibits the expression of HIF1alpha and/or HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide. The antisense oligonucleotide comprises at least one modified internucleoside linkage, preferably a phosphorothioate linkage. It also comprises at least one modified sugar moiety, preferably a 2'-O-

CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further comprises at least one modified nucleobase, preferably a 5-methylcytosine. The antisense oligonucleotides are useful for the treatment of diseases such as hyperproliferative disorders, e.g. cancer, preferably a cancer carrying a p53 mutation, or an angiogenic disorder that affects the eye. The compound is also useful for treating tumours, CC hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis, CC atherosclerosis and smooth muscle cell proliferation in the blood vessels CC such as stenosis or restenosis following angioplasty. It is also useful CC in drug discovery and target validation, and can be utilised for CC diagnostics, therapeutics, prophylaxis and as research reagents and kits. CC The present sequence represents an antisense oligonucleotide used in the CC examples of the present invention.

XX  
SQ Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 90.0%; Score 18; DB 13; Length 20;  
XX  
Best Local Similarity 100.0%; Pred. No. 24;  
XX  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGAGCCACGAGTCCAA 20  
DB ( 1 TGAGCCACGAGTCCAA 18)

RESULT 5  
ADZ58028/c  
ID ADZ58028 standard; RNA; 19 BP.  
XX  
AC ADZ58028/  
XX  
DT 30-JUN-2005 (first entry)  
XX  
DE Sense siRNA oligo that modulates human HIF1 expression Seq 156.  
XX  
KM ss; short interfering RNA; siRNA; gene silencing; RNA interference;  
KM hypoxia inducible factor 1; cancer; hyperproliferation;  
KM macular degeneration; diabetic retinopathy; cytostatic; ophthalmological;  
KM antidiabetic.  
XX  
OS Homo sapiens.  
XX  
PN WO2005035759-A2.  
XX  
PD 21-APR-2005.  
XX  
PF 20-AUG-2004; 2004WO-US027294.  
XX  
PR 20-AUG-2003; 2003US-0496655P.  
PR 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 03-DEC-2003; 2003US-00727780.  
PR 14-JAN-2004; 2004US-00757780.  
PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-00780447.  
PR 16-APR-2004; 2004US-00826366.  
PR 30-APR-2004; 54US-09997777.  
PR 24-MAY-2004; 54US-09996666.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Ueman N, Mcswiggen J;  
XX  
DR WPI; 2005-306364/31.  
XX  
PT New chemically synthesized double stranded short interfering nucleic acid molecule that directs cleavage of a hypoxia inducible factor 1 RNA via RNA interference (RNAi), useful for modulating HIF1, its expression or activity.  
XX  
PS Claim 33; SEQ ID NO 156; 189pp; English.  
XX  
CC This invention relates to a novel chemically synthesized double stranded

CC short interfering nucleic acid strand (siRNA). Specifically, it refers to  
CC siRNAs that direct cleavage of a hypoxia inducible factor 1 (HIF1) RNA via  
CC RNA interference (RNAi). In particular, the siRNAs may include short  
CC interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA)  
CC and short hairpin RNA (shRNA) molecules that are capable of mediating  
CC RNAi. The present invention describes a sense strand of a double-stranded  
CC siRNA that comprises a nucleotide sequence that is complementary to HIF1  
CC RNA or a portion thereof, and where a second strand is the complementary  
CC antisense siRNA strand. Note that the sense region is connected to the  
CC antisense region via a polynucleotide linker molecule. Accordingly, these  
CC siRNAs are useful in providing compositions for the treatment of traits,  
CC diseases and conditions that respond to modulation of HIF1 expression,  
CC namely cancer and proliferative conditions including macular  
CC degeneration, diabetic retinopathy and other conditions associated with  
CC hypoxia inducible proliferation. As such, these compositions exhibit  
CC cytostatic, ophthalmological and antidiabetic activities. This  
CC oligonucleotide sequence is a sense siRNA strand that targets human HIF1  
CC RNA to modulate expression given in an exemplification of the invention.  
XX  
SQ Sequence 19 BP; 3 A; 5 C; 6 G; 0 T; 5 U; 0 Other;  
Query Match 87.0%; Score 17.4; DB 14; Length 19;  
Best Local Similarity 94.7%; Pred. No. 49;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
1 AATGAGCCACCACTGTCCA 19  
Db 19 AGTGAGCCACCACTGTCCA 1  
XX  
RESULT 6  
AD258248  
ID AD258248 standard; RNA; 19 BP.  
XX  
AC AD258248;  
XX  
DT 30-JUN-2005 (first entry)  
XX  
DE Antisense siRNA oligo that modulates human HIF1 expression Seq 376.  
XX  
XX  
XX ss; short interfering RNA; siRNA; gene silencing; RNA interference;  
XX hypoxia inducible factor 1; cancer; hyperproliferation;  
XX macular degeneration; diabetic retinopathy; cytostatic; ophthalmological;  
XX antidiabetic; antisense.  
XX  
XX Homo sapiens.  
XX  
XX WO2005035759-A2.  
XX  
XX 21-APR-2005.  
XX  
XX 20-AUG-2004; 2004MO-US027294.  
XX  
XX 20-AUG-2003; 2003US-0496655P.  
XX 23-OCT-2003; 2003US-00693059.  
XX 24-NOV-2003; 2003US-00720448.  
XX 03-DEC-2003; 2003US-00727780.  
XX 14-JAN-2004; 2004US-00757803.  
XX 10-FEB-2004; 2004US-0543480P.  
XX 13-FEB-2004; 2004US-00780447.  
XX 16-APR-2004; 2004US-00826966.  
XX 30-APR-2004; 54US-09997777.  
XX 24-MAY-2004; 54US-09996666.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
XX Ueman N, Mcswigen J;  
XX  
XX WPI; 2005-306364/31.  
XX  
XX New chemically synthesized double stranded short interfering nucleic acid  
XX molecule that directs cleavage of a hypoxia inducible factor 1 RNA via  
XX RNA interference (RNAi), useful for modulating HIF1, its expression or

PT activity.  
XX  
XX Claim 33; SEQ ID NO 376; 189bp; English.  
XX  
XX This invention relates to a novel chemically synthesized double stranded  
XX short interfering nucleic acid strand (siRNA). Specifically, it refers to  
XX siRNAs that direct cleavage of a hypoxia inducible factor 1 (HIF1) RNA via  
XX RNA interference (RNAi). In particular, the siRNAs may include short  
XX interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA)  
XX and short hairpin RNA (shRNA) molecules that are capable of mediating  
XX RNAi. The present invention describes a sense strand of a double-stranded  
XX siRNA that comprises a nucleotide sequence that is complementary to HIF1  
XX RNA or a portion thereof, and where a second strand is the complementary  
XX antisense siRNA strand. Note that the sense region is connected to the  
XX antisense region via a polynucleotide linker molecule. Accordingly, these  
XX siRNAs are useful in providing compositions for the treatment of traits,  
XX diseases and conditions that respond to modulation of HIF1 expression,  
XX namely cancer and proliferative conditions including macular  
XX degeneration, diabetic retinopathy and other conditions associated with  
XX hypoxia inducible proliferation. As such, these compositions exhibit  
XX cytostatic, ophthalmological and antidiabetic activities. This  
XX oligonucleotide sequence is an antisense siRNA strand that targets human  
XX HIF1 RNA to modulate expression given in an exemplification of the  
XX invention.  
XX  
SQ Sequence 19 BP; 5 A; 6 C; 5 G; 0 T; 3 U; 0 Other;  
Query Match 87.0%; Score 17.4; DB 14; Length 19;  
Best Local Similarity 78.9%; Pred. No. 49;  
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
XX  
1 AATGAGCCACCACTGTCCA 19  
Db 1 AGTGAGCCACCACTGTCCA 19  
XX  
RESULT 7  
AB283188/c  
ID AB283188 standard; DNA; 32 BP.  
XX  
AC AB283188;  
XX  
DT 14-MAY-2003 (first entry)  
XX  
XX Toxicologically relevant human PCR primer #347.  
XX  
XX Toxicologically relevant gene; toxicological response; PCR primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX Synthetic.  
XX  
XX WO2003016500-A2.  
XX  
XX 27-FEB-2003.  
XX  
XX 16-AUG-2002; 2002MO-US026514.  
XX 16-AUG-2001; 2001US-0313080P.  
XX  
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.  
XX  
XX Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweiser K;  
XX Allen P;  
XX  
XX WPI; 2003-268322/26.  
XX  
XX Determining a toxicological response to an agent, useful for screening of  
XX drugs, comprises comparing the expression profile of one or more human  
XX toxic response genes to a reference gene expression profile indicative of  
XX toxicity.  
XX  
XX Claim 1; Page 129; 455pp; English.

CC The present invention describes a method (M1) for determining a  
 CC toxicological response to an agent, which comprises comparing the  
 CC expression profile of one or more human toxic response genes to a  
 CC reference gene expression profile indicative of toxicity, and so  
 CC determining the presence of a toxic response to the agent. Also  
 CC described: (1) an array comprising one or more polynucleotides selected  
 CC from the genes corresponding to the partial sequences given in AB282842  
 CC to AB284764, or their fragments of at least 20 nucleotides, or homologues  
 CC ; and (2) determining if a gene putatively identified to be a toxic  
 CC response gene plays a role on toxic response pathways by determining the  
 CC expression profile of the gene after exposure of cells or a human subject  
 CC to a known toxic pharmaceutical or industrial agent, comprising: (a)  
 CC exposing cells to an agent or isolating cells from a human subject who  
 CC was exposed to an agent; (b) obtaining the test gene expression profile  
 CC for a putatively identified toxic response gene after exposure to a known  
 CC toxic pharmaceutical or industrial agent; and (c) comparing the test  
 CC profile to the expression profile of a gene with a similar function or  
 CC comparing the test profile to the expression profile of that gene after  
 CC exposure to other known toxic compounds. The methods are useful for  
 CC predicting and determining toxicological responses on a cellular, organ  
 CC or system level. The arrays comprising the human genes are useful for  
 CC toxicological screening of drugs, pharmaceutical compounds and chemicals  
 CC XX

Seq Sequence 32 BP, 5 A; 11 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 10; Length 32;  
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTC 18  
 DB 28 AGTAGCCACCACTGTC 11

RESULT 8  
 AEB68623/c  
 AEB68623 standard; DNA; 20 BP.

AC AEB68623;

DT 06-OCT-2005 (first entry)

Mouse glucocorticoid receptor antisense oligonucleotide SEQ ID NO:243.

antisense oligonucleotide; glucocorticoid receptor; antidiabetic;  
 anorectic; diabetes; obesity; syndrome X; hyperglycemia; hyperlipidemia;  
 ss; phosphorothioate; 2'-O-methoxyethyl; 2'-MOE.

OS Mus sp.

Key Location/Qualifiers

FT modified\_base 1..20  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate backbone, all cytosine residues  
 are 5-methylcytosines"

FT modified\_base 1..5  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT 16..20  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"

PN US2005164271-A1.

PD 28-JUL-2005.

PF 20-JAN-2005; 2005US-00039629.

XX 20-JAN-2004; 2004US-0538173P.  
 PR 03-MAR-2004; 2004US-0550191P.

XX (BHAN/) BHANOT S.  
 PA (DOBI/) DOBIE K W.  
 PA (FREI/) FREIER S M.  
 PA (DEAN/) DEAN N M.  
 PA (BEN/) BENNETT C F.  
 PI Bhanc S, Dobie KM, Freier SM, Dean NM, Bennett CF;  
 DR WPI; 2005-521414/53.  
 XX

PT New antisense compound targeted to a nucleic acid molecule encoding  
 PT glucocorticoid receptor, useful for modulating the expression of  
 PT glucocorticoid receptor, or for treating or diagnosing, e.g. diabetes or  
 PT obesity.

XX Claim 18; SEQ ID NO 243; 129pp; English.

XX The invention relates to an antisense compound 13-80 nucleobases in  
 CC length targeted to a nucleic acid molecule encoding glucocorticoid  
 CC receptor, where the compound is complementary to the nucleic acid  
 CC molecule encoding glucocorticoid receptor, and where the compound  
 CC inhibits the expression of glucocorticoid receptor mRNA. Also described:  
 CC (1) a method of inhibiting the expression of glucocorticoid receptor in a  
 CC cell or tissue; (2) a method of treating an animal having a disease or  
 CC condition associated with glucocorticoid receptor; (3) a method of  
 CC decreasing blood glucose levels in an animal; and (4) a method of  
 CC preventing or delaying the onset of an increase in blood lipid levels in  
 CC an animal. The compounds, compositions, and methods are useful for  
 CC modulating the expression of glucocorticoid receptor. They are also  
 CC useful for the diagnosis and treatment of diseases and conditions  
 CC associated with glucocorticoid receptor, e.g. diabetes (Type 2), obesity,  
 CC metabolic syndrome X, hyperglycemia, or hyperlipidemia. The present  
 CC sequence represents a mouse glucocorticoid receptor chimeraic  
 CC phosphorothioate antisense oligonucleotide, which is used in an example  
 CC from the present invention.

Seq Sequence 20 BP, 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 14; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 1.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAACCAACCACTGCCAA 20  
 DB 19 TGAACCAACCACTGCCAA 2

RESULT 9  
 AEF79634/c  
 ID AEF79634 standard; DNA; 20 BP.

AC AEF79634;

DT 06-APR-2006 (first entry)

Mouse glucocorticoid receptor antisense oligonucleotide, SEQ:243.

antisense therapy; obesity; anorectic; diabetes;  
 non-insulin dependent diabetes; hyperglycemia; antidiabetic; syndrome X;  
 hypercholesterolemia; antilipemic; metabolic; glucocorticoid receptor;  
 antisense oligonucleotide; phosphorothioate; ss.

OS Mus musculus.

Key Location/Qualifiers

FT modified\_base 1..20  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "This oligonucleotide has a phosphorothioate  
 backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'  
 and 3' ends, which are 5 nucleotides in length. Also all  
 cytosine residues are 5-methylcytosines"

XX US2006025373-A1.  
 XX  
 XX 02-FEB-2006.  
 XX  
 XX 18-AUG-2005; 2005US-00207478.  
 XX  
 XX 20-JAN-2004; 2004US-0538173P.  
 XX 03-MAR-2004; 2004US-0550191P.  
 XX 20-JAN-2005; 2005US-00039629.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 XX  
 XX Bhanot S, Dobie KM, Freter SM;  
 XX WPI; 2006-117670/12.  
 XX  
 XX New antisense compound 8-80 nucleobases in length targeted to a nucleic  
 XX acid molecule encoding glucocorticoid receptor, useful for treating a  
 XX disease or condition mediated by glucocorticoid expression, e.g.  
 XX diabetes, or obesity.  
 XX  
 XX Example 13; SEQ ID NO 243; 128bp; English.  
 XX  
 XX The invention relates to antisense oligonucleotides targeted to the  
 XX glucocorticoid receptor gene, which inhibit its expression. The invention  
 XX also relates to the use of these antisense oligonucleotides in methods  
 XX for inhibiting glucocorticoid receptor expression; for reducing blood  
 XX glucose, triglyceride, cholesterol or insulin levels; for increasing  
 XX insulin sensitivity; for inhibiting hepatic glucose output; or for  
 XX reducing body fat mass. The glucocorticoid receptor (encoded on human  
 XX chromosome 5q11-q13) is a ubiquitously expressed cytoplasmic member of  
 XX the nuclear hormone superfamily of receptors. It is responsible for  
 XX mediating the effects of glucocorticoids on various physiological  
 XX functions e.g., stimulation of gluconeogenesis, decreased glucose uptake  
 XX and utilization in peripheral tissues, increased glycogen deposition,  
 XX suppression of immune and inflammatory responses, inhibition of cytokine  
 XX synthesis, and acceleration of various developmental events. Stress-  
 XX induced elevation of glucocorticoid synthesis and release can lead to  
 XX adverse health effects resulting from, amongst other responses, increased  
 XX cytokine synthesis and increased glucose production. Inhibition of  
 XX glucocorticoid receptor expression may therefore be useful in the  
 XX treatment of diseases resulting from glucocorticoid activity. Antisense  
 XX oligonucleotides targeted to the glucocorticoid receptor gene are useful  
 XX for the treatment of obesity, diabetes (particularly type 2 diabetes),  
 XX metabolic syndrome X, hyperglycemia and hyperlipidemia (especially  
 XX elevated blood cholesterol or triglyceride levels). The present sequence  
 XX represents a phosphorothioate antisense oligonucleotide targeted to mouse  
 XX glucocorticoid receptor RNA.  
 XX  
 XX Sequence 20 BP; 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;  
 XX  
 XX Query Match 74.0%; Score 14.8; DB 15; Length 20;  
 XX Best Local Similarity 88.9%; Pred. No. 1.1e+03;  
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX QY 3 TGAAGCACCAAGTCCAA 20  
 XX 19 TGAACCAACAGTCCCAA 2  
 XX  
 XX RESULT 10  
 XX ADE53245/c  
 XX ID ADE53245 standard; DNA; 43 BP.  
 XX  
 XX AC ADE53245;  
 XX  
 XX DT 29-JUN-2004 (first entry)  
 XX  
 XX XX FEN-1 related DNA used within the scope of the invention, #379.  
 XX DB FEN-1 related DNA used within the scope of the invention, #379.  
 XX  
 XX KM Flap endonuclease-1; FEN-1; endonuclease; structure-specific nuclease;

KW invasive cleavage structure; thermostable; DNA polymerase; 5' nuclease;  
 KW viral infection; bacterial infection; cancer; forensic analysis;  
 KM paternity determination; ds.  
 XX  
 XX OS Methanocaldococcus jannaschii.  
 XX  
 XX MO20020755-A2.  
 XX  
 XX 12-SEP-2002.  
 XX  
 XX 15-NOV-2001; 2001WO-US044953.  
 XX  
 XX 15-NOV-2000; 2000US-00713601.  
 XX 17-NOV-2000; 2000US-00714935.  
 XX  
 XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 XX Lyamichev VI, Kaiser MW, Lyamicheva N;  
 XX WPI; 2002-750464/81.  
 XX  
 XX New composition useful for detecting and characterizing nucleic acid  
 XX sequences and sequence variants for detecting the presence of viral or  
 XX bacterial infections or cancer, comprises purified or chimerical FEN-1  
 XX endonuclease.  
 XX  
 XX Example 65; SEQ ID NO 427; 871bp; English.  
 XX  
 XX The invention discloses a new composition (I) which comprises a purified  
 XX flap endonuclease-1 (FEN-1) from e.g. *Sulfolobus solfataricus*,  
 XX *Pyrobaculum aerophilum* or a chimerical FEN-1 endonuclease having a  
 XX portion of the above endonuclease in addition to that of *Pyrococcus*  
 XX *horikoshii* and *Aeropyrum pernix*. Also claimed is a composition comprising  
 XX an isolated nucleic acid sequence encoding the endonuclease mentioned  
 XX above, a composition comprising a vector having the nucleic acid sequence  
 XX cited above, a composition comprising a host cell and vector cited above,  
 XX a mixture comprising a first structure-specific nuclease selected from  
 XX the species mentioned in composition (I), and a purified second structure  
 XX -specific nuclease and detecting a target sequence, comprising: (a)  
 XX providing a sample suspected of containing the target sequence,  
 XX oligonucleotides capable of forming an invasive cleavage structure in the  
 XX presence of the target sequence, and a FEN-1 endonuclease selected from  
 XX the species cited above and (b) exposing the sample to the  
 XX oligonucleotides and FEN-1 endonuclease. The second structure-specific  
 XX nuclease also comprises a thermostable DNA polymerase. It has a 5'  
 XX nuclease derived from a DNA polymerase altered in amino acid sequence  
 XX such that it exhibits reduced DNA synthetic activity from that of the  
 XX wild-type DNA polymerase but retains substantially the same 5' nuclease  
 XX activity of the wild-type DNA polymerase. The second structure is  
 XX selected from CLEAVASE BN enzyme, CLEAVASE DA enzyme, CLEAVASE DN enzyme,  
 XX CLEAVASE DV enzyme, CLEAVASE BN/thrombin enzyme, CLEAVASE TTHDN enzyme,  
 XX T. aquaticus DNA polymerase, T. thermophilus DNA polymerase, E. coli Exo  
 XX III and S. cerevisiae Rad1/Rad10 complex. The nucleic acid treatment kit  
 XX comprises (i) and oligonucleotides capable of forming an invasive  
 XX cleavage structure in the presence of a target nucleic acid. The  
 XX oligonucleotides comprise: (a) a first oligonucleotide having a 5'  
 XX portion complementary to a first portion of a target nucleic acid and (b)  
 XX a second oligonucleotide comprising a 5' portion complementary to a  
 XX second portion of the target nucleic acid downstream of and contiguous to  
 XX the first portion and a 3' portion. The 3' portion of the second  
 XX oligonucleotide comprises a single 3' terminal nucleotide not  
 XX complementary to the target nucleic acid. Additionally, the kit has a  
 XX third oligonucleotide complementary to a third portion of the target  
 XX nucleic acid upstream of the first portion of the first target nucleic  
 XX acid. In detecting a target sequence, the oligonucleotides and  
 XX endonuclease are mixed under conditions where an invasive cleavage  
 XX structure is formed between the target sequence and the oligonucleotides  
 XX if the target sequence is present in the sample, where the invasive  
 XX cleavage structure is cleaved by the endonuclease to form a cleavage  
 XX product. The composition is useful in detecting and characterizing  
 XX specific nucleic acid sequences and sequence variants which can be used  
 XX in detecting the presence of viral or bacterial infections, and other  
 XX diseases such as cancer. The composition may also be used in forensic

CC analysis or for paternity determinations. The sequence presented is a FEN  
CC -1 related DNA used within the scope of the invention.  
XX  
SQ Sequence 43 BP; 12 A; 13 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 6; Length 43;  
Best Local Similarity 88.9%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 TGAGCCACGAGTTCGA 20  
DB 32 TGAGCCACGAGTTCGA 15

RESULT 11  
AC145528/c  
ID AC145528 standard; RNA; 21 BP.

AC AC145528;

XX 24-MAR-2005 (first entry)

XX CDH6 siRNA antisense sequence. SEQ ID 6600.

XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;  
XX short interfering RNA; gene silencing.

XX Synthetic.

XX WO2005001092-A2.

XX 06-JAN-2005.

XX 19-MAY-2004; 2004MO-US015645.

XX 20-MAY-2003; 2003US-0471729P.

XX (AMHP) WYETH.

XX Be X, Wei L, Slonim DK, Howes SH;

XX WPI; 2005-075568/08.

XX Pharmaceutical composition comprising an agent capable of modulating an  
XX expression level or protein activity of a gene, e.g. ABC4, or a T cell  
XX activated by the polypeptide or antibody, and a carrier, useful for  
XX treating cancer.

XX Claim 3; SEQ ID NO 6600; 113pp; English.

XX The present invention relates to a novel pharmaceutical composition  
XX comprising: (a) an agent capable of modulating an expression level or  
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene  
XX; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
XX (b) a carrier. The pharmaceutical composition may also comprise a  
XX polynucleotide capable of inhibiting or decreasing the expression of the  
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
XX invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
XX pharmaceutical composition is useful for treating cancer, e.g. colon  
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a  
XX CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic form directly from WIPO at  
XX ftp://ipo.int/pub/published\_pot\_sequences

XX Sequence 21 BP; 5 A; 4 C; 7 G; 0 T; 5 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 14; Length 21;  
Best Local Similarity 84.2%; Pred. No. 2.3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACGAGTTCGA 19  
DB 21 AATGAGCCACCTGTCTTCA 3

RESULT 12  
AAT80533/c  
ID AAT80533 standard; DNA; 25 BP.

XX AAT80533;

XX 25-MAR-2003 (revised)

XX 04-NOV-1997 (first entry)

XX Pichia pastoris genomic DNA PCR primer.

XX Isozymes; genomic clone; methanol-regulated promoter; yeast; starch;  
XX ethanol; regulatory region; polymerase chain reaction; ss.

XX Synthetic.

XX US5641661-A.

XX 24-JUN-1997.

XX 25-MAR-1994; 94US-00220606.

XX 25-MAR-1993; 93US-00037617.

XX 25-MAR-1993; 93US-00037618.

XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.

XX Sverlow CG, Kumagai MH;

XX WPI; 1997-340945/31.

XX Conversion of starch to ethanol using recombinant yeast - which contain  
XX starch-degrading enzyme coding sequence under the control of Pichia ZZAI  
XX promoter.  
XX Example 6; Col 17; 46pp; English.

XX A novel method has been produced for converting starch to ethanol. The  
XX method involves growing yeast cells in a culture medium, where the yeast  
XX cells contain a genetic construct comprising a nucleotide sequence  
XX encoding a starch-degrading enzyme under the control of a ZZAI promoter  
XX (the promoter of a Pichia pastoris alcohol oxidase gene). The present  
XX sequence represents a PCR primer used in the amplification of Pichia  
XX pastorie genomic DNA. The ZZAI promoter can direct high-level expression  
XX of the rice alpha-amylase gene in Saccharomyces cerevisiae. (Updated on  
XX 25-MAR-2003 to correct PF field.)

XX Sequence 25 BP; 4 A; 6 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 2; Length 25;  
Best Local Similarity 84.2%; Pred. No. 2.3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 ATGAGCCACGAGTTCGA 20  
DB 19 ATGAGCCACGAGTTCGA 1

RESULT 13  
AAK87554/c  
ID AAK87554 standard; DNA; 25 BP.

XX AAK87554;

XX 08-OCT-1999 (first entry)

XX Pichia pastoris alcohol oxidase PCR primer.



KM Gene function; protein function; alcohol oxidase; PCR; primer; AOX1 gene;  
 KM ss.  
 XX  
 OS Synthetic.  
 OS Pichia pastoris.  
 XX WO9936516-A2.  
 XX  
 PD 22-JUL-1999.  
 XX  
 PF 15-JAN-1999; 99WO-US001164.  
 XX  
 PR 16-JAN-1998; 98US-00008186.  
 XX  
 PA (BIO-) BIOSOURCE TECHNOLOGIES INC.  
 XX Della-Cioppa G, Erwin RL, Fitzmaurice WP, Hanley KM, Kumagai MH,  
 PI Lindo JA, McGee DR, Padgett HS, Pogue GP,  
 XX WPI; 1999-458459/38.  
 XX  
 PT Determining the function of polynucleotide sequences and their encoded  
 PT proteins by transfecting them into a host organism.  
 XX  
 PS Example 8; Page 57; 156pp; English.  
 XX  
 CC This primer corresponds to the nucleotide sequence of the Pichia pastoris  
 CC alcohol oxidase AOX1 gene promoter. It was used in the PCR amplification  
 CC of P. pastoris cDNA. Expression in transfected Nicotiana benthamiana  
 CC plants confirmed that the yeast cDNA encoded alcohol oxidase. The  
 CC invention provides methods for rapidly determining the function of  
 CC nucleic acid sequences by transfecting them into a host organism to  
 CC effect expression, and analyzing the resulting phenotypic and biochemical  
 CC changes. Methods for silencing endogenous genes, for selecting desired  
 CC functions of RNAs and proteins, and for inhibiting an endogenous protease  
 CC in a plant host are also provided  
 XX  
 SQ Sequence 25 BP; 4 A; 6 C; 6 G; 9 T; 0 U; 0 Other;  
 XX  
 QY Query Match 71.0%; Score 14.2; DB 2; Length 25;  
 Best Local Similarity 84.2%; Pred. No. 2.3e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 DB 2 ATGAGCCACCAAGTGTCCA 20  
 19 ATGAGCCACCAAGTGTCCA 1  
 XX  
 RESULT 14  
 ACP58076/c  
 ID ACP58076 standard; DNA; 20 BP.  
 XX  
 AC ACP58076;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Human PRDX3 gene fragment C chip analysis 5' primer.  
 XX  
 KM PRDX3; tumour; peroxiredoxin 3; cytosolic; gene therapy; chip analysis;  
 KM chromatin immunoprecipitation; PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003087312-A2.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 08-APR-2003; 2003WO-US010539.  
 XX  
 PR 08-APR-2002; 2002US-0370873P.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX

PI Dang CV, Monsey D;  
 XX  
 DR WPI; 2003-845314/78.  
 XX  
 PT Inhibiting tumor growth by delivering to a tumor cell, expressing an mRNA  
 PT molecule complementary to native Peroxiredoxin 3 (PRDX3) mRNA, an  
 PT antisense construct comprising 15 or 19 nucleotides of a murine or human  
 PT PRDX3 cDNA.  
 XX  
 PS Claim 24; Page 23; 0pp; English.  
 XX  
 CC The invention relates to inhibiting tumour growth. The method involves  
 CC delivering to a tumour cell an antisense construct comprising at least 15  
 CC or 19 nucleotides of a murine or human Peroxiredoxin 3 (PRDX3) cDNA,  
 CC where the tumour cell expresses an mRNA molecule that is complementary to  
 CC native PRDX3 mRNA. The method is useful for inhibiting tumour growth.  
 CC Sequences ACP58074-91 represent primers used in real-time PCR for chip  
 CC (chromatin immunoprecipitation) analysis of human PRDX3 genomic DNA  
 XX  
 SQ Sequence 20 BP; 3 A; 5 C; 8 G; 4 T; 0 U; 0 Other;  
 XX  
 QY Query Match 70.0%; Score 14; DB 10; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 4 GAGCCACCAAGTGTTC 17  
 18 GAGCCACCAAGTGTTC 5  
 XX  
 RESULT 15  
 ADG77414/c  
 ID ADG77414 standard; DNA; 24 BP.  
 XX  
 AC ADG77414;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Canine disease marker-related PCR primer 258.  
 XX  
 KM genetic disease; genetic trait; dog; carrier of recessive disease;  
 KM copper toxicosis; CT; canine genome map; breed-specific profile;  
 KM DNA fingerprint; dog identification; PCR; primer; ss.  
 XX  
 OS Canis familiaris.  
 XX  
 PN WO9731011-A1.  
 XX  
 PD 28-AUG-1997.  
 XX  
 PF 18-FEB-1997; 97WO-US002396.  
 XX  
 PR 22-FEB-1996; 96US-0012060P.  
 XX  
 PA (UNMI ) UNIV MICHIGAN.  
 PA (UNMS ) UNIV MICHIGAN STATE.  
 XX  
 PI Brewer GU, Venta PJ, Yuzbasiyan-Gurkan V;  
 XX  
 DR WPI; 1997-435082/40.  
 XX  
 PT New oligonucleotide primers for diagnosis of genetic diseases and traits  
 PT in dogs - amplify specific regions of the genome containing  
 PT microsatellite repeats, especially for diagnosing copper toxicosis and  
 PT carriers.  
 XX  
 PS Claim 1; Page 14; 40pp; English.  
 XX  
 CC This invention relates to novel oligonucleotide PCR primers which may be  
 CC used to identify markers associated with genetic diseases and traits in  
 CC dogs, in particular to diagnose genetic diseases that are not  
 CC phenotypically visible and to identify carriers of recessive disease. A  
 CC specific application is diagnosis of copper toxicosis (CT). The invention

CC can also be used to create a genetic map of the canine genome; to  
 CC generate breed-specific profiles; to establish paternity and to identify  
 CC dogs from DNA fingerprints. The method provides rapid analysis of the  
 CC target sequences from only a small sample of DNA. Diagnosis can be done  
 CC at any time in the dog's life. The present sequence is that of a PCR  
 CC primer of the invention.

XX Sequence 24 BP; 6 A; 3 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAGT 14  
 |||||  
 Db 20 AATGAGCCACCAGT 7

Search completed: May 21, 2006, 22:31:24  
 Job time : 388 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:49:17 ; Search time 2196 Seconds  
(without alignments)  
509.284 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20  
Sequence: 1 aatgagccaccagctgcacaa 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 194034

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_hic:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_g8a1:\*  
12: gb\_g8a2:\*  
13: gb\_g8a3:\*  
14: gb\_g8a4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.6	68.0	50	1	AU104418 AU104418
C 2	13.6	68.0	50	12	CC571047 CH240_446
C 3	13.2	66.0	47	11	AZ588937 IM0397M06
C 4	13.2	66.0	50	10	DY245677 CSTBQ1D11
C 5	12.8	64.0	19	11	AZ601003 IM0419M06
C 6	12.8	64.0	46	2	BG389655 602415101
C 7	12.8	64.0	46	2	BG389736 602415101
C 8	12.6	63.0	49	13	CL518330 DNE1D11 F
C 9	12.2	61.0	35	13	CZ194627 PST2762-N
C 10	12.2	61.0	38	11	AZ438336 IM0228E19
C 11	12	60.0	40	1	AI689673 tx95h04.x
C 12	12	60.0	46	1	AI65872 me48b09.r
C 13	12	60.0	49	13	AI629100 wj38f09.x
C 14	12	60.0	50	10	TS1051 yb71d09.x
C 15	11.8	59.0	33	10	TS1051 yb71d09.x
C 16	11.8	59.0	37	1	AA984865 am62b07.g
C 17	11.8	59.0	37	1	AI327021 m394f07.x
C 18	11.8	59.0	42	10	DY243241 CSTBP1802
C 19	11.8	59.0	42	10	DY243241 CSTBP1802

20	11.8	59.0	46	1	AA109130	AA109130 mp38h07.r
C 21	11.8	59.0	49	1	AA995990	AA995990 os13h03.s
C 22	11.8	59.0	49	1	AI453675	AI453675 c128h04.x
C 23	11.6	58.0	29	14	AG188890	AG188890 Pan t10g1
C 24	11.6	58.0	40	1	AI318261	AI318261 cb03a09.x
C 25	11.6	58.0	42	11	AZ687147	AZ687147 2M0177E21
C 26	11.6	58.0	46	14	TA121G07Q	AL463047 T. brucei
C 27	11.4	57.0	23	5	CF298913	CF298913 71EAF--02
C 28	11.4	57.0	37	10	W70797	W70797 me44b08.r1
C 29	11.4	57.0	41	1	AA679912	AA679912 ac85c06.s
C 30	11.4	57.0	47	11	AZ783950	AZ783950 2M026D08
C 31	11.4	57.0	47	14	CT178809	CT178809 Sue scroef
C 32	11.4	57.0	50	14	CR175859	CR175859 Forward s
C 33	11.2	56.0	30	11	AZ503721	AZ503721 IM0343A11
C 34	11.2	56.0	31	14	TA216A03Q	AL479849 T. brucei
C 35	11.2	56.0	35	11	AZ308154	AZ308154 IM0010D19
C 36	11.2	56.0	35	14	BX893619	BX893619 Arabidops
C 37	11.2	56.0	38	14	TA170A06Q	AL474162 T. brucei
C 38	11.2	56.0	40	14	BX124349	BX124349 Danio rer
C 39	11.2	56.0	42	12	CC885727	CC885727 SALK 1477
C 40	11.2	56.0	43	13	CL982875	CL982875 GC0096 T1
C 41	11.2	56.0	44	11	AZ598581	AZ598581 IM0413P22
C 42	11.2	56.0	47	10	DY246292	DY246292 CSTBQ1E02
C 43	11.2	56.0	49	7	AV960480	AV960480 AV960480
C 44	11.2	56.0	50	1	AU106035	AU106035 AU106035
C 45	11.2	56.0	50	2	BG370398	BG370398 na133a04.

#### ALIGNMENTS

RESULT 1	AU104418/c	50 bp	RNA	linear	EST 28-JAN-2004
LOCUS	AU104418				
DEFINITION	AU104418 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone				
ACCESSION	HEP22673				
VERSION	AU104418.1	GI:13553939			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 50)				
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Oca,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.				
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites				
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)				
COMMENT	11375929				
FEATURES	Location/Qualifiers				
source	1..50				
	/organism="Homo sapiens"				
	/mol_type="RNA"				
	/db_xref="taxon:9606"				
	/clone="HEP22673"				
ORIGIN	/clone_lib="Sugano Homo sapiens cDNA library"				
Query Match	68.0%; Score 13.6; DB 1; Length 50;				

Best Local Similarity 80.0%; Pred. No. 8.2e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCAA 20  
DB 35 AATGAGCCACCACTGTCCAA 16

## RESULT 2

CC571047 50 bp DNA linear GSS 18-JUN-2003  
LOCUS CH240\_446F14.T7 CHORI-240 Bos taurus genomic clone CH240\_446F14,  
DEFINITION genomic survey sequence.

ACCESSION CC571047  
VERSION CC571047.1 GI:31908316  
KEYWORDS GSS.  
SOURCE Bos taurus (cattle)  
ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 50)  
Holt, R., Stott, J., Yang, G., Barber, S., Smalhus, D., Prabhhu, A.-L.,  
Teal, M., Cloutier, A., Lee, D., Gilm, N., Olson, T., Mayo, M.,  
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,  
Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,  
Schein, J., Marra, M., de Jong, P., Keeler, J.W., and Kappes, S.M.  
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478  
Unpublished (2003)  
Other GSSs: CH240\_446F14.TARBA13P2  
Contact: Rob Holt

TITLE Sequencing  
JOURNAL The British Columbia Cancer Agency Genome Science Centre  
COMMENT 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6  
Tel: 604-877-6085  
Fax: 604-877-6276  
Email: rholt@bccsc.ca

Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm). This work  
was undertaken as part of the International Bovine BAC Mapping  
Consortium (IBMC) by CSIRO Livestock Industries, Australia and the  
British Columbia Genome Sciences Centre, Canada.  
Plate: 446 row: F column: 14  
Seg primer: T7  
Class: BAC ends.

## FEATURES

Location/Qualifiers  
1..50  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="Bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_446F14"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_11b="CHORI-240"  
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull 11 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 68.0%; Score 13.6; DB 12; Length 50;

Best Local Similarity 80.0%; Pred. No. 8.2e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCAA 20  
DB 29 AATGAGCCACCACTGTCCAA 10

RESULT 3

AZ588937/c 47 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0357M06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0357M06 R, genomic survey sequence.

ACCESSION AZ588937  
VERSION AZ588937.1 GI:11711127  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.  
1 (bases 1 to 47)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5605  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0397 row: M column: 06  
Seg primer: CACACAGAAACAGCATGACCC  
Class: plasmid ends  
High quality sequence stop: 47.  
Location/Qualifiers  
1..47  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0357M06"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_11b="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42ny; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## FEATURES

Location/Qualifiers  
1..47  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0357M06"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_11b="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42ny; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 66.0%; Score 13.2; DB 11; Length 47;

Best Local Similarity 83.3%; Pred. No. 1.3e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AATGAGCCACCACTGTCCAA 19  
DB 38 AATGAGCCACCACTGTCCAA 21

RESULT 4  
DY245677/c 50 bp mRNA linear EST 06-FEB-2006  
LOCUS CSTB01D1177A\_0\_50 CST-BM Mus musculus cDNA, mRNA sequence.  
DEFINITION DY245677  
VERSION DY245677.1 GI:86581321  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 50)  
Bowman,T.V., McCooley,A.J., Merchant,A.A., Ramos,C.A., Fonseca,P.,  
Pindexter,A., Bradfield,S.B., Oliveira,D.M., Green,R., Zheng,Y.,  
Jackson,K.A., Chambers,S.M., McKinney-Freeman,S.U., Norwood,K.G.,  
Dillington,G., Gunaratne,P.H., Steffen,D. and Goodell,M.A.  
Differential mRNA Processing in Hematopoietic Stem Cells  
Stem Cells (2006) In press  
Contact: Goodell MA  
Center for Cell and Gene Therapy  
Baylor College of Medicine  
One Baylor Plaza, Houston, TX 77030, USA  
Tel: 713 798 1265  
Fax: 713 798 1230  
Email: goodell@bcm.edu.  
location/Qualifiers  
1..50  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone\_lib="CST-BM"  
/note="Organ: Bone Marrow; A hematopoietic stem cell gene  
depleted library prepared by Suppression Subtractive  
Hybridization of whole bone marrow cells subtracted with  
side population cells from bone marrow. Prepared as a  
control for the CST-HSC library. cDNAs were fragmented,  
concatenated, cloned, sequenced, and electronically  
de-concatenated."

ORIGIN  
Query Match 66.0%; Score 13.2; DB 10; Length 50;  
Best Local Similarity 83.3%; Pred. No. 1.3e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 TGAGCCACCAAGTGTCCA 20  
|||||  
24 TGAGCACCCGTGACCA 7  
Db

RESULT 5  
AZ601003 19 bp DNA linear GSS 13-DEC-2000  
LOCUS IM0419M06P Mouse 10kb plasmid UGCLM library Mus musculus genomic  
DEFINITION clone UGCLM0419M06 F, genomic survey sequence.  
VERSION AZ601003  
ACCESSION AZ601003.1 GI:11723193  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Ielam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D. Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0419 row: M column: 06  
Seq primer: CATTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
location/Qualifiers  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCLM0419M06"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCLM library"  
/note="Vector: pMD22uv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g1473214[gb|AF129072.1]), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN  
Query Match 64.0%; Score 12.8; DB 11; Length 19;  
Best Local Similarity 87.5%; Pred. No. 1.8e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 ATGAGCCACCAAGTGT 17  
|||||  
Db 1 ATGACACCAAGTGT 16

RESULT 6  
BG389655 46 bp mRNA linear EST 12-MAR-2001  
LOCUS 602415001P1 NIH\_MGC\_92 Homo sapiens cDNA clone IMAGE:4523400 5',  
DEFINITION mRNA sequence.  
VERSION BG389655  
ACCESSION BG389655.1 GI:13283103  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
1 (bases 1 to 46)  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

DNA sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
 Plate: LLM10426 row: a column: 01  
 High quality sequence stop: 46.  
 Location/Qualifiers

## FEATURES

source

1. 46  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4523400"  
 /issue\_type="embryonal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 92"  
 /note="Organ: testis; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 2.5 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 64.0%; Score 12.8; DB 2; Length 46;  
 Best Local Similarity 87.5%; Pred. No. 2e+05;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AATGAGCCACCATGT 16  
 |||||  
 Db 3 ACTGAGCCACCATGT 18

RESULT 7 46 bp mRNA linear EST 12-MAR-2001  
 BG389736  
 LOCUS 60241510.F1 NIH\_MGC\_92 Homo sapiens cDNA clone IMAGE:4523401 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG389736 GI:13283172  
 VERSION BG389736.1 GI:13283172  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 1 (bases 1 to 46)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strauberg, Ph.D.  
 Email: [csapbs-remail.nih.gov](mailto:csapbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
 Plate: LLM10426 row: a column: 02  
 High quality sequence stop: 46.  
 Location/Qualifiers

## FEATURES

source

1. 46  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4523401"  
 /issue\_type="embryonal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 92"  
 /note="Organ: testis; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 2.5 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 64.0%; Score 12.8; DB 2; Length 46;  
 Best Local Similarity 87.5%; Pred. No. 2e+05;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AATGAGCCACCATGT 16  
 |||||  
 Db 3 ACTGAGCCACCATGT 18

RESULT 8 49 bp DNA linear GSS 02-APR-2004  
 CL518330  
 LOCUS DBR101 Planking Sequence Tag of Oryza sativa T-DNA insertion lines  
 DEFINITION Oryza sativa (japonica cultivar-group) genomic, genomic survey  
 sequence.  
 ACCESSION CL518330  
 VERSION CL518330.1 GI:46145130  
 KEYWORDS GSS.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BRP  
 clade; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 49)  
 Salland, C., Gay, C., Larmande, P., Bes, M., Piffanel, P., Piegau, B.,  
 Proc, G., Regad, F., Bourgeois, E., Neyraud, D., Petit, C.,  
 Ghesquiere, A., Delzeny, M., Glaesmann, J.C. and Guiderdoni, E.  
 High throughput T-DNA insertion mutagenesis in rice: A first step  
 towards in silico reverse genetics  
 plant J. (2004) In press  
 Contact: Guiderdoni  
 UMR PIA Biotrop program  
 CIRAD  
 TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE  
 Tel: 33467615629  
 Fax: 33467615605  
 Email: [emmanuel.guiderdoni@cirad.fr](mailto:emmanuel.guiderdoni@cirad.fr)  
 Class: T-DNA tagged.  
 Location/Qualifiers

## FEATURES

source

1. 49  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="genomic DNA"  
 /cultivar="Nipponbare"  
 /db\_xref="taxon:39947"  
 /clone\_lib="Planking Sequence Tag of Oryza sativa T-DNA  
 insertion lines"  
 /note="PCR was performed on DNA of primary transformants  
 of Oryza sativa plants. The DNA fragment(s) resulting of  
 PCR were directly sequenced from the left border to  
 determine the genomic sequence flanking the insertion.  
 T-DNA derived sequences were removed. Information to order  
 the corresponding mutant line and a link to a database  
 providing a graphical display is available from June 2004  
 at <http://genoplante-info.infobiogen.fr/oryzatagline/>.  
 This sequence has been generated in the framework of the  
 French plant genomics program Genoplante  
 (<http://www.genoplante.org> and  
<http://genoplante-info.infobiogen.fr>)."

## ORIGIN

Query Match 63.0%; Score 12.6; DB 13; Length 49;  
 Best Local Similarity 78.9%; Pred. No. 2.6e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AATGAGCCACCATGTCCA 19  
 |||||  
 Db 11 AATGAGCAACCATGTACA 29

RESULT 9  
 CZ194627/c

University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddum@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0228 row: E column: 19  
Seq primer: CGTGTGTAACAGCGCCACTG  
Class: plasmid ends  
High quality sequence stop: 38.

FEATURES

Source

location/Qualifiers

1..38

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="MGCIM0228B1.9"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_id="Mouse 10kb plasmid UNGCM library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMP42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 61.0%; Score 12.2; DB 11; Length 38;  
Best Local Similarity 82.4%; Pred. No. 4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Gy 2 ATGAGCCACCAAGTCCTC 18  
|||||||  
Db 17 ATGGCCACCACTGCC 1

RESULT\_11

A1689673 40 bp mRNA linear EST 27-MAY-1999  
t395f04.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2277367 3'  
similar to SW:CA21 CHICK P02467 PROCOLLAGEN ALPHA 2(I) CHAIN  
PRECURSOR, contains MER22.c3 MSRI repetitive element ;, mRNA  
sequence.

ACCESSION A1689673 GI:4900967  
VERSION A1689673.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 40)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.

JOURNAL

COMMENT

Email: cgabbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:  
 www.bio.linn.gov/bbrp/image/image.html

Trace considered overall poor quality  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

## FEATURES

source

1. 40  
 /organization="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2277367"  
 /tissue\_type="serous papillary carcinoma, high grade, 2 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_1lb="NCI\_CGAP\_Ut4"  
 /note="Organ: uterus; Vector: PCMV-SPORT6; Site\_1: Salt; Site\_2: NCI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"

## ORIGIN

Query Match 60.0%; Score 12; DB 1; Length 40;  
 Best Local Similarity 75.0%; Pred. No. 5e+05;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATGAGCCACGATGTCGAA 20  
 16 AAGGAGCCAAAGGTCGAA 35

Db

## RESULT 12

AA165872

LOCUS 46 bp mRNA linear EST 19-DEC-1996  
 DEFINITION me48509.t1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus  
 CDNA clone IMAGE:614777 5' similar to TR:G295543 G295543 AFRICAN  
 CLAIMED FROG BETA-TRCP. ; mRNA sequence.

ACCESSION AA165872  
 VERSION AA165872.1 GI:1744331

KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 46)  
 Marx, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Stepec, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.

## AUTHORS

## TITLE

JOURNAL

COMMENT

Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LINL; contact the  
 IMAGE Consortium (info@image.linn.gov) for further information.  
 MGI:375601  
 Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -28M13 rev1 from Amersham

High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 46  
 /organization="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:614777"  
 /tissue\_type="embryo"  
 /dev\_stage="13.5dpc embryos"  
 /lab\_host="DH10B"  
 /clone\_1lb="Life Tech mouse embryo 13 5dpc 10666014"  
 /note="Organ: whole embryo; Vector: PCMV-SPORT2; Site\_1: Salt; Site\_2: NCI; Cloned unidirectionally. Primer: Oligo dt. 13.5dpc embryos. PCMV-SPORT2 vector."

## FEATURES

source

## ORIGIN

Query Match 60.0%; Score 12; DB 1; Length 46;  
 Best Local Similarity 75.0%; Pred. No. 5.1e+05;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATGAGCCACGATGTCGAA 20  
 17 ATTGAGCAATAGATGTCGAA 36

Db

## RESULT 13

AI829100/C

LOCUS 49 bp mRNA linear EST 21-DEC-1999  
 DEFINITION wj38f09.x1 NCI CGAP Lu19 Homo sapiens CDNA clone IMAGE:2405129 3'  
 similar to SW:ADP2\_HUMAN P30041 ANTIOXIDANT PROTEIN 2 ; mRNA  
 sequence.

ACCESSION AI829100.1 GI:5449771  
 VERSION AI829100  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 1 (bases 1 to 49)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

## COMMENT

CDNA Library Preparation: M. Benito Soares, Ph.D.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:  
 www.bio.linn.gov/bbrp/image/image.html

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 Seq primer: -40UP from Gibco  
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## FEATURES

source

1. 49  
 /organization="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2405129"  
 /tissue\_type="squamous cell carcinoma, poorly differentiated (4 pooled tumors, including primary and metastatic)"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_1lb="NCI\_CGAP\_Lu19"  
 /note="Organ: lung; Vector: pT7T3D-Pac1; 1st strand cDNA



was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

Query Match 60.0%; Score 12; DB 1; Length 49;  
Best Local Similarity 100.0%; Pred. No. 5.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACCAAGTCCA 19  
|||  
24 CACCAAGTCCA 13

RESULT 14  
CM273788/c 50 bp DNA linear GSS 31-OCT-2004  
LOCUS 104.746.11404087.148.35366.024 Sorghum methylation filtered library  
DEFINITION (L15ID: 104) Sorghum bicolor genomic clone 11404087, genomic survey  
sequence.

ACCESSION CM273788  
VERSION CM273788.1 GI:54989976  
KEYWORDS GSS.  
SOURCE Sorghum bicolor (sorghum)  
ORGANISM Sorghum bicolor

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 50)

AUTHORS Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holman, H., Roe, B.A., Wiley, G., Korf, I.P., Rabinowicz, P.D., Lakey, N., McComble, W.R., Jeddeloh, J.A. and Martensen, R.A.  
Sorghum genome sequencing by methylation filtration  
Proc Biol. 3 (1), e13 (2005)

TITLE P108 Biol. 3 (1), e13 (2005)  
JOURNAL 15660154  
COMMENT Contact: Bedell JA  
Orion Genomics, LLC  
4041 Forest Park Ave, St. Louis, MO 63108, USA  
Tel: 314 615 6979  
Fax: 314 615 5975  
Email: jbedell@oriongenomics.com  
Plate: 746 row: 1 column: 07  
Seq primer: SWfor Forward  
Class: methylation filtered  
High quality sequence stop: 50.

FEATURES  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
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/clone\_1ib="Sorghum methylation filtered library (L15ID: 104)"  
/note="Organ: leaf; Vector: pBCSK(-); Site 1: HindIII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HindIII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN  
Query Match 60.0%; Score 12; DB 13; Length 50;  
Best Local Similarity 75.0%; Pred. No. 5.2e+05;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATGAGCCACGATGTCGA 20

Db 31 AGTACGACTACCTCTCCA 12

RESULT 15  
LOCUS T51051  
DEFINITION T51051 30 bp mRNA linear EST 06-FEB-1995  
YP71009.1 Striatagene ovary (#937217) Homo sapiens cDNA clone  
IMAGE:76625 5' similar to similar to gp:K16865 ELONGATION FACTOR  
1-ALPHA 1 (HUMAN), mRNA sequence.

ACCESSION T51051  
VERSION T51051.1 GI:652911  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 30)

REFERENCE Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favell, A., Glen, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Scheinberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevasaki, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)

TITLE Contact: Wilson RK  
JOURNAL 8889549  
COMMENT Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
Insert Size: 576

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Source: IMAGE Consortium, LINT This clone is available royalty-free through LINT; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
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/sex="female"  
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/clone\_1ib="Striatagene ovary (#937217)"  
/note="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Total ovary tissue, normal, caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGACG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

ORIGIN  
Query Match 59.0%; Score 11.8; DB 10; Length 30;  
Best Local Similarity 86.7%; Pred. No. 6.1e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGAGCCACGATG 15  
|||  
Db 2 AATGAGCCACGATG 16

Search completed: May 21, 2006, 23:02:45  
Job time: 2200 secs



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 22:08:44 ; Search time 115.5 Seconds  
(without alignments)  
324.002 Million cell updates/sec

Title: US-10-766-185-2

Sequence: 1 aatgagccacagtgccaa 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1429044

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

Issued Patents NA:\*

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- 2: /EMC\_Celerra\_SIDS3/prodata/2/ina/5\_COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/ina/6\_COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/ina/7\_COMB.seq:\*
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- 7: /EMC\_Celerra\_SIDS3/prodata/2/ina/10\_COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/prodata/2/ina/11\_COMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/prodata/2/ina/12\_COMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/prodata/2/ina/13\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.4	92.0	37	US-09-579-897-2	Sequence 2, Appl1
2	14.2	71.0	25	US-08-220-606B-13	Sequence 13, Appl1
3	14	70.0	25	US-09-396-196G-97802	Sequence 97802, A
4	14	70.0	25	US-09-396-196G-97803	Sequence 97803, A
5	14	70.0	25	US-09-396-196G-97804	Sequence 97804, A
6	14	70.0	25	US-09-396-196G-97805	Sequence 97805, A
7	13.8	69.0	41	US-09-330-235-3	Sequence 3, Appl1
8	13.4	67.0	25	US-09-396-196G-99591	Sequence 99591, A
9	13.4	67.0	25	US-09-396-196G-99592	Sequence 99592, A
10	13.4	67.0	25	US-09-396-196G-99593	Sequence 99593, A
11	13.2	66.0	20	US-09-661-753-66	Sequence 66, Appl1
12	13.2	66.0	22	US-09-316-392B-208	Sequence 208, Appl1
13	13.2	66.0	25	US-09-396-196G-60900	Sequence 60900, A
14	13.2	66.0	25	US-09-396-196G-60901	Sequence 60901, A
15	13.2	66.0	50	US-10-131-827-6025	Sequence 6025, Ap
16	13.2	66.0	50	US-10-131-831-6025	Sequence 6025, Ap
17	13	65.0	25	US-09-396-196G-97819	Sequence 97819, A
18	12.8	64.0	20	US-10-131-827-9040	Sequence 9040, Ap
19	12.8	64.0	25	US-09-396-196G-50633	Sequence 50633, A
20	12.8	64.0	25	US-09-396-196G-57705	Sequence 57705, A
21	12.8	64.0	25	US-09-396-196G-114077	Sequence 114077, A
22	12.8	64.0	25	US-09-396-196G-114078	Sequence 114078, A
23	12.8	64.0	25	US-09-396-196G-114079	Sequence 114079, A

24	12.8	64.0	25	US-09-396-196G-115388	Sequence 115388, A
25	12.8	64.0	38	US-08-857-946-79	Sequence 79, Appl1
26	12.8	64.0	38	US-08-857-946-79	Sequence 10994, A
27	12.6	63.0	25	US-09-396-196G-10994	Sequence 10994, A
28	12.6	63.0	25	US-09-396-196G-10084	Sequence 10084, A
29	12.6	63.0	25	US-09-396-196G-10389	Sequence 10389, A
30	12.6	63.0	25	US-09-396-196G-10389	Sequence 10389, A
31	12.6	63.0	25	US-09-396-196G-10389	Sequence 10389, A
32	12.6	63.0	50	US-10-131-827-608	Sequence 608, Appl1
33	12.6	63.0	50	US-10-131-831-608	Sequence 608, Appl1
34	12.4	62.0	20	US-08-116-389-9	Sequence 9, Appl1
35	12.4	62.0	20	US-08-708-431-9	Sequence 9, Appl1
36	12.4	62.0	20	US-08-880-830-9	Sequence 9, Appl1
37	12.4	62.0	20	US-09-860-473-55	Sequence 55, Appl1
38	12.4	62.0	20	PCT-US94-13895-9	Sequence 9, Appl1
39	12.4	62.0	22	US-08-855-810-34	Sequence 34, Appl1
40	12.4	62.0	23	US-08-116-389-10	Sequence 10, Appl1
41	12.4	62.0	23	US-08-708-431-10	Sequence 10, Appl1
42	12.4	62.0	23	US-08-880-830-10	Sequence 10, Appl1
43	12.4	62.0	23	PCT-US94-13895-10	Sequence 10, Appl1
44	12.4	62.0	25	US-08-997-685A-13	Sequence 13, Appl1
45	12.4	62.0	25	US-09-086-436-1	Sequence 1, Appl1

#### ALIGNMENTS

```

RESULT 1
US-09-579-897-2
; Sequence 2, Application US/09579897
; Patent No. 6432927
; GENERAL INFORMATION:
; APPLICANT: Gregory, Richard
; APPLICANT: Vincent, Karen
; TITLE OF INVENTION: Compositions and Methods for Inducing Gene Expression
; FILE REFERENCE: GA0112CIP2
; CURRENT APPLICATION NUMBER: US/09/579,897
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/067,546
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/25753
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 09/133,612
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-579-897-2

Query Match          92.0%; Score 18.4; DB 3; Length 37;
Best Local Similarity 95.0%; Pred. No. 3.5;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY      1 AATGACCCACAGTGCCAA 20
DB      8 AATGACCCACAGTGCCAA 27

RESULT 2
US-08-220-606B-13/c
; Sequence 13, Application US/08220606B
; Patent No. 5641661
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Monto H.
; APPLICANT: Genadi, Sverlow J.
; TITLE OF INVENTION: Pichia Pastoris Alcohol Oxidase Z2A1 and
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Penie & Edmonds

```

STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/220,606B  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Halliuh, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 8129-065  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA  
US-08-220-606B-13

Query Match 71.0%; Score 14.2; DB 2; Length 25;  
Best Local Similarity 84.2%; Pred. No. 5.3e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGAGCCACGAGTGTCCA 20  
DB 19 ATGAGCCACGAGTGTCCA 1

RESULT 3  
US-09-396-196G-97802/c  
Sequence 97802, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 97802  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-97802

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Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCCACCAAGTGTCCA 19  
DB 25 GCCACCAAGTGTCCA 12

RESULT 4

US-09-396-196G-97803/c  
Sequence 97803, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 97803  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-97803

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Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCCACCAAGTGTCCA 19  
DB 23 GCCACCAAGTGTCCA 10

RESULT 5  
US-09-396-196G-97804/c  
Sequence 97804, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 97804  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-97804

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Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCCACCAAGTGTCCA 19  
DB 22 GCCACCAAGTGTCCA 9

RESULT 6  
US-09-396-196G-97805/c  
Sequence 97805, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 97805  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-97805

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Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCCACCACTGTCCA 19  
DB 20 GCCACCACTGTCCA 7

RESULT 7  
US-09-330-235-3/C  
Sequence 3, Application US/09330235  
Patent No. 6459018  
GENERAL INFORMATION:  
APPLICANT: Knutson, Debbie  
TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS  
FILE REFERENCE: WOCO.156.00US  
CURRENT APPLICATION NUMBER: US/09/330,235  
CURRENT FILING DATE: 1999-06-10  
PRIOR APPLICATION NUMBER: 60/089,043  
PRIOR FILING DATE: 1998-06-12  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patent Version 3.0  
SEQ ID NO 3  
LENGTH: 41  
TYPE: DNA  
ORGANISM: synthetic primer  
US-09-330-235-3

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Best Local Similarity 88.2%; Pred. No. 9.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTTC 17  
DB 34 AATGAGCCACCACTGTTC 18

RESULT 8  
US-09-396-196G-99591  
Sequence 99591, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 99591  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-99591

Query Match 67.0%; Score 13.4; DB 3; Length 25;  
Best Local Similarity 93.3%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGCCCACTGTGTCCA 19  
DB 11 AGCCCACTGTGTCCA 25

RESULT 9  
US-09-396-196G-99592  
Sequence 99592, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 99592  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-99592

Query Match 67.0%; Score 13.4; DB 3; Length 25;  
Best Local Similarity 93.3%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGCCCACTGTGTCCA 19  
DB 5 AGCCCACTGTGTCCA 19

RESULT 10  
US-09-396-196G-99593  
Sequence 99593, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 99593  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-99593

Query Match 67.0%; Score 13.4; DB 3; Length 25;  
Best Local Similarity 93.3%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGCCCACTGTGTCCA 19  
DB 2 AGCCCACTGTGTCCA 16

RESULT 11  
US-09-661-753-66/C  
Sequence 66, Application US/09661753  
Patent No. 6436909  
GENERAL INFORMATION:  
APPLICANT: Nicholas M. Dean  
APPLICANT: Susan F. Murray  
TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA  
FILE REFERENCE: ISPH-0438  
CURRENT APPLICATION NUMBER: US/09/661,753  
CURRENT FILING DATE: 2000-09-14  
EARLIER APPLICATION NUMBER: 60/154,546  
EARLIER FILING DATE: 1999-09-17  
NUMBER OF SEQ ID NOS: 68  
SEQ ID NO 66  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-661-753-66

Query Match 66.0%; Score 13.2; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGAGCCACCACTGTCCA 19  
DB 19 ATGAGCTACTCTGGTCCA 2

RESULT 12  
US-09-216-393B-208/C  
Sequence 208, Application US/09216393B  
Patent No. 6514694  
GENERAL INFORMATION:  
APPLICANT: Mulhausen, Michael James  
TITLE OF INVENTION: TOXOPLASMA GONDI PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: TX-1-C2  
CURRENT APPLICATION NUMBER: US/09/216,393B  
CURRENT FILING DATE: 1998-12-18  
PRIOR APPLICATION NUMBER: 08/994,825  
PRIOR FILING DATE: 1997-12-19  
NUMBER OF SEQ ID NOS: 366  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 208  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Primer  
US-09-216-393B-208

Query Match 66.0%; Score 13.2; DB 3; Length 22;  
Best Local Similarity 83.3%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGAGCCACCACTGTCCA 19  
DB 21 ATGATGACACCACTGTCCA 4

RESULT 13  
US-09-396-196G-60900  
Sequence 60900, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 60900  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-60900

Query Match 66.0%; Score 13.2; DB 3; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGAGCCACCACTGTCCA 19  
DB 5 ATGAGCTACTCTGGTCCA 22

RESULT 14  
US-09-396-196G-60901  
Sequence 60901, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 60901  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-60901

Query Match 66.0%; Score 13.2; DB 3; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGAGCCACCACTGTCCA 19  
DB 2 ATGAGCTACTCTGGTCCA 19

RESULT 15  
US-10-131-827-6025/C  
Sequence 6025, Application US/10131827  
Patent No. 6905827  
GENERAL INFORMATION:  
APPLICANT: Wohlgenuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE DISEASES  
FILE REFERENCE: 506612000120  
CURRENT APPLICATION NUMBER: US/10/131,827  
CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: US 10/006,290  
PRIOR FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: US 60/296,764  
PRIOR FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 9090



GenCore version 5.1.8  
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OM nucleic - nucleic search, using bw model

Run on: May 21, 2006, 22:09:18 ; Search time 654 Seconds  
(without alignments)  
375.769 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagccaccagtgcacaa 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24111450

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US11\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US11\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US11C\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	20	8 US-10-766-185-1	Sequence 1, Appli
C 2	20	100.0	20	8 US-10-766-185-2	Sequence 2, Appli
C 3	18.4	92.0	37	6 US-10-190-394-2	Sequence 187, Appli
C 4	18	90.0	20	9 US-10-719-370A-187	Sequence 187, App
C 5	16.4	82.0	19	14 US-11-083-784-1242584	Sequence 225584,
C 6	16.4	82.0	19	15 US-11-101-244-1242584	Sequence 225584,
C 7	16	80.0	24	11 US-10-310-914A-185175	Sequence 195175,
C 8	15.8	79.0	25	9 US-10-719-900-515021	Sequence 515021,
C 9	15.8	79.0	25	15 US-11-121-849-650902	Sequence 650902,
C 10	15.4	77.0	25	8 US-10-719-956-334675	Sequence 334675,
C 11	15.4	77.0	25	9 US-10-719-900-571979	Sequence 571979,
C 12	15.4	77.0	25	15 US-11-121-849-650903	Sequence 650903,
C 13	15.2	76.0	25	15 US-11-121-849-655975	Sequence 655975,
C 14	14.8	74.0	19	14 US-11-083-784-1242371	Sequence 1242371,
C 15	14.8	74.0	19	14 US-11-101-244-1242371	Sequence 1242371,
C 16	14.8	74.0	20	13 US-11-039-629-243	Sequence 243, App
C 17	14.8	74.0	20	16 US-11-207-476-243	Sequence 243, App

18	14.8	74.0	25	8 US-10-719-956-517759	Sequence 517759,
C 19	14.8	74.0	25	9 US-10-719-900-289663	Sequence 289663,
C 20	14.8	74.0	25	9 US-10-719-900-417993	Sequence 417993,
C 21	14.8	74.0	25	9 US-10-719-900-852952	Sequence 852952,
C 22	14.8	74.0	25	13 US-11-036-317-724065	Sequence 724065,
C 23	14.8	74.0	43	9 US-10-783-557-428	Sequence 428, App
C 24	14.4	72.0	19	14 US-11-083-784-1242405	Sequence 1242405,
C 25	14.4	72.0	19	14 US-11-083-784-1242405	Sequence 1242405,
C 26	14.4	72.0	19	15 US-11-101-244-1242405	Sequence 1242405,
C 27	14.4	72.0	19	15 US-11-101-244-1242405	Sequence 1242405,
C 28	14.4	72.0	25	8 US-10-719-956-583062	Sequence 583062,
C 29	14.4	72.0	25	8 US-10-719-956-604657	Sequence 604657,
C 30	14.4	72.0	25	9 US-10-719-900-7136	Sequence 7136, Ap
C 31	14.4	72.0	25	9 US-10-719-900-299394	Sequence 299394,
C 32	14.4	72.0	25	9 US-10-719-900-589698	Sequence 589698,
C 33	14.4	72.0	25	13 US-11-036-317-195619	Sequence 195619,
C 34	14.4	72.0	25	13 US-11-036-317-228611	Sequence 228611,
C 35	14.4	72.0	25	13 US-11-036-317-239617	Sequence 239617,
C 36	14.4	72.0	25	13 US-11-036-317-268109	Sequence 268109,
C 37	14.4	72.0	25	13 US-11-036-317-314795	Sequence 314795,
C 38	14.4	72.0	25	13 US-11-036-317-358459	Sequence 358459,
C 39	14.4	72.0	25	13 US-11-036-317-578460	Sequence 578460,
C 40	14.4	72.0	25	13 US-11-060-756-134735	Sequence 134735,
C 41	14.4	72.0	25	15 US-11-121-849-412943	Sequence 412943,
C 42	14.2	71.0	21	10 US-10-847-918-6500	Sequence 6500, Ap
C 43	14.2	71.0	24	11 US-10-310-914A-28845	Sequence 28845, A
C 44	14.2	71.0	25	6 US-10-072-438-17	Sequence 17, Appl
C 45	14.2	71.0	25	6 US-10-137-765-32	Sequence 32, Appl

## ALIGNMENTS

RESULT 1  
US-10-766-185-1/c  
Sequence 1, Application US/10766185  
Publication No. US20040152655A1  
GENERAL INFORMATION:  
APPLICANT: Yoon, Heejeong  
APPLICANT: Ahn, Chang Ho  
APPLICANT: Lee, Young Bok  
APPLICANT: Mao, Lingjun  
APPLICANT: Jiang, Xiaoming  
TITLE OR INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1  
FILE REFERENCE: REX 7034  
CURRENT APPLICATION NUMBER: US/10/766,185  
CURRENT FILING DATE: 2004-01-28  
NUMBER OF SEQ ID NOS: 130  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 20  
TYPE: DNA  
ORGANISM: human  
US-10-766-185-1

Query Match  
Best Local Similarity 100.0%; Score 20; DB 8; Length 20;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCACTGTCCAA 20  
Db 20 AATGAGCCACCACTGTCCAA 1

RESULT 2  
US-10-766-185-2  
Sequence 2, Application US/10766185  
Publication No. US20040152655A1  
GENERAL INFORMATION:  
APPLICANT: Yoon, Heejeong  
APPLICANT: Ahn, Chang Ho  
APPLICANT: Lee, Young Bok  
APPLICANT: Mao, Lingjun



APPLICANT: Jiang, Xiaoming  
TITLE OF INVENTION: Antisense oligonucleotides that inhibit expression of HIF-1  
FILE REFERENCE: REX 7034  
CURRENT APPLICATION NUMBER: US/10/766,185  
CURRENT FILING DATE: 2004-01-28  
NUMBER OF SEQ ID NOS: 130  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 20  
TYPE: DNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: antisense oligonucleotide  
US-10-766-185-2

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTCCAA 20  
DB 1 AATGAGCCACCAAGTCCAA 20

RESULT 3  
US-10-190-394-2  
Sequence 2, Application US/10190394  
Publication No. US20030018007A1  
GENERAL INFORMATION:  
APPLICANT: Gregory, Richard  
APPLICANT: Vincent, Karen  
TITLE OF INVENTION: Compositions and Methods for Inducing Gene  
TITLE OF INVENTION: Expression  
FILE REFERENCE: GA0112CIP2  
CURRENT APPLICATION NUMBER: US/10/190,394  
CURRENT FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: US/09/579,897  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/067,546  
PRIOR FILING DATE: 1997-12-04  
PRIOR APPLICATION NUMBER: PCT/US98/25753  
PRIOR FILING DATE: 1998-12-04  
PRIOR APPLICATION NUMBER: 09/133,612  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 37  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-190-394-2

Query Match 92.0%; Score 18.4; DB 6; Length 37;  
Best Local Similarity 95.0%; Pred. No. 29;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTCCAA 20  
DB 8 AGTGAGCCACCAAGTCCAA 27

RESULT 4  
US-10-719-370A-187  
Sequence 187, Application US/10719370A  
Publication No. US20040220393A1  
GENERAL INFORMATION:  
APPLICANT: Ward, Donna T.  
APPLICANT: Dobie, Kenneth W.  
APPLICANT: Marcussen, Eric G.  
APPLICANT: Freiler, Susan W.  
TITLE OF INVENTION: MODULATION OF HIF1A AND HIF2A EXPRESSION  
FILE REFERENCE: ISPT-1010  
CURRENT APPLICATION NUMBER: US/10/719,370A

CURRENT FILING DATE: 2003-11-21  
PRIOR APPLICATION NUMBER: US 10/304,126  
PRIOR FILING DATE: 2002-11-23  
NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 187  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Construct  
US-10-719-370A-187

Query Match 90.0%; Score 18; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGAGCCACCAAGTCCAA 20  
DB 1 TGAGCCACCAAGTCCAA 18

RESULT 5  
US-11-083-784-225584/C  
Sequence 225584, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Pharmacia, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 225584  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-225584

Query Match 82.0%; Score 16.4; DB 14; Length 19;  
Best Local Similarity 94.4%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTCC 18  
DB 18 AGTGAGCCACCAAGTCC 1

RESULT 6  
US-11-101-244-225584/C  
Sequence 225584, Application US/1101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Pharmacia, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 225584  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-719-900-515021

Query Match 82.0%; Score 16.4; DB 15; Length 19;  
Best Local Similarity 94.4%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCC 18  
Db 18 AGTGAGCCACCAAGTGTCC 1

RESULT 7  
US-10-310-914A-195175  
Sequence 195175, Application US/10310914A  
Publication No. US2006000322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087, 0200, CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 138402  
SOFTWARE: Patent in version 3.3  
SEQ ID NO 195175  
LENGTH: 24  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-195175

Query Match 80.0%; Score 16; DB 11; Length 24;  
Best Local Similarity 87.5%; Pred. No. 5e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGCCACCAAGTGTCCA 20  
Db 1 AGCCACCAAGTGTCCA 16

RESULT 8  
US-10-719-900-515021/C  
Sequence 515021, Application US/10719900  
Publication No. US2005002616A1  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528.1  
CURRENT APPLICATION NUMBER: US/10/719,900  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,808  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 515021  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-515021

Query Match 79.0%; Score 15.8; DB 9; Length 25;

Best Local Similarity 89.5%; Pred. No. 6.3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AATGAGCCACCAAGTGTCCA 19  
Db 21 AATGAGCCACCAAGTGTCCA 3

RESULT 9  
US-11-121-849-650902/C  
Sequence 650902, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 650902  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-121-849-650902

Query Match 79.0%; Score 15.8; DB 15; Length 25;  
Best Local Similarity 89.5%; Pred. No. 6.3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCA 19  
Db 23 AATGAGCCACCAAGTGTCCA 5

RESULT 10  
US-10-719-956-334675/C  
Sequence 334675, Application US/10719956  
Publication No. US20040146910A1  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
FILE REFERENCE: 3527.1  
CURRENT APPLICATION NUMBER: US/10/719,956  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,836  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 699466  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 334675  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-10-719-956-334675

Query Match 77.0%; Score 15.4; DB 8; Length 25;  
Best Local Similarity 94.1%; Pred. No. 1e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCC 17  
Db 17 AATGAGCCACCAAGTGTCC 1

RESULT 11  
US-10-719-900-571979/C  
Sequence 571979, Application US/10719900  
Publication No. US2005002616A1  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou

;; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
;; FILE REFERENCE: 3528.1  
;; CURRENT APPLICATION NUMBER: US/10/719,900  
;; CURRENT FILING DATE: 2003-11-20  
;; PRIOR APPLICATION NUMBER: 60/427,808  
;; PRIOR FILING DATE: 2002-11-20  
;; NUMBER OF SEQ ID NOS: 982914  
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
;; SEQ ID NO 571979  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: Mus musculus  
US-10-719-900-571979

Query Match 77.0%; Score 15.4; DB 9; Length 25;  
Best Local Similarity 94.1%; Pred. No. 1e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGCCACCACTGTCCA 19  
Db 19 TGAGCCACCACTGTCCA 3

RESULT 12  
US-11-121-849-650903/C  
; Sequence 650903, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 650903  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-650903

Query Match 77.0%; Score 15.4; DB 15; Length 25;  
Best Local Similarity 94.1%; Pred. No. 1e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCACTGTTC 17  
Db 18 AATGAGCCACCACTGTAC 2

RESULT 13  
US-11-121-849-655975  
; Sequence 655975, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 655975  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-655975

Query Match 76.0%; Score 15.2; DB 15; Length 25;  
Best Local Similarity 85.0%; Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCACTGTCCA 20  
Db 1 AATGAGCCACCACTGTACCA 20

RESULT 14  
US-11-083-784-1242371  
; Sequence 1242371, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1242371  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1242371

Query Match 74.0%; Score 14.8; DB 14; Length 19;  
Best Local Similarity 72.2%; Pred. No. 2.1e+03;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AATGAGCCACCACTGTCCA 19  
Db 2 AATGAGCCACCAUGUCUA 19

RESULT 15  
US-11-101-244-1242371  
; Sequence 1242371, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1242371  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1242371

US-11-101-244-1242371

Query Match 74.0%; Score 14.8; DB 15; Length 19;

Best Local Similarity 72.2%; Pred. No. 2.1e+03;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATGAGCCACCAAGTGTCCA 19  
|:|||||:|:  
Db 2 AUGAGCCACCAUGUCUA 19

Search completed: May 21, 2006, 22:32:02  
Job time : 656 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: May 21, 2006, 22:18:38 / Search time 32.5 Seconds  
(without alignments)  
43.419 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20  
Sequence: 1 aatgagccacagtgtccaa 20

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 387544

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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2: /EMC\_Celextra\_SIDS3/ptocdata/2/pubpna/US06\_NEW\_PUB.seq:\*  
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8: /EMC\_Celextra\_SIDS3/ptocdata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	25	US-11-217-529-13735	Sequence 13735, A
2	13.2	66.0	25	US-11-217-529-44186	Sequence 44186, A
3	13.2	66.0	25	US-11-217-529-86968	Sequence 86968, A
4	13.2	66.0	50	US-10-511-937-2733	Sequence 2733, Ap
5	13	65.0	25	US-11-217-529-74193	Sequence 74193, A
6	13	65.0	25	US-11-217-529-88752	Sequence 88752, A
7	12.8	64.0	25	US-11-217-529-9748	Sequence 9748, Ap
8	12.8	64.0	25	US-11-217-529-117069	Sequence 117069, A
9	12.6	63.0	25	US-11-217-529-22469	Sequence 22469, A
10	12.6	63.0	25	US-11-217-529-71644	Sequence 71644, A
11	12.6	63.0	25	US-11-217-529-125526	Sequence 125526, A
12	12.4	62.0	25	US-11-217-529-8089	Sequence 8089, Ap
13	12.4	62.0	25	US-11-217-529-45366	Sequence 45366, A
14	12.2	61.0	25	US-11-217-529-29471	Sequence 29471, A
15	12.2	61.0	25	US-11-217-529-38860	Sequence 38860, A
16	12.2	61.0	25	US-11-217-529-44089	Sequence 44089, A
17	12.2	61.0	25	US-11-217-529-89698	Sequence 89698, A
18	12.2	61.0	25	US-11-217-529-110177	Sequence 110177, A
19	12.2	61.0	25	US-11-217-529-132345	Sequence 132345, A
20	12.2	61.0	25	US-11-217-529-159967	Sequence 159967, A
21	12.2	61.0	26	US-11-257-502-110	Sequence 110, App
22	12	60.0	25	US-11-217-529-30855	Sequence 30855, A
23	12	60.0	25	US-11-217-529-38629	Sequence 38629, A
24	12	60.0	25	US-11-217-529-43480	Sequence 43480, A
25	12	60.0	25	US-11-217-529-56109	Sequence 56109, A

26	12	60.0	25	US-11-217-529-62922	Sequence 62922, A
27	12	60.0	25	US-11-217-529-90441	Sequence 90441, A
28	12	60.0	25	US-11-217-529-100966	Sequence 100966, A
29	12	60.0	25	US-11-217-529-133723	Sequence 133723, A
30	12	60.0	25	US-11-217-529-135675	Sequence 135675, A
31	12	60.0	25	US-11-217-529-155061	Sequence 155061, A
32	12	60.0	25	US-11-217-529-160487	Sequence 160487, A
33	12	60.0	25	US-11-217-529-166036	Sequence 166036, A
34	12	60.0	25	US-11-217-529-189912	Sequence 189912, A
35	12	60.0	25	US-11-217-529-189916	Sequence 189916, A
36	11.8	59.0	20	US-10-511-937-861	Sequence 861, App
37	11.8	59.0	25	US-11-217-529-25957	Sequence 25957, A
38	11.8	59.0	25	US-11-217-529-33050	Sequence 33050, A
39	11.8	59.0	25	US-11-217-529-34973	Sequence 34973, A
40	11.8	59.0	25	US-11-217-529-57598	Sequence 57598, A
41	11.8	59.0	25	US-11-217-529-64579	Sequence 64579, A
42	11.8	59.0	25	US-11-217-529-104375	Sequence 104375, A
43	11.8	59.0	25	US-11-217-529-141696	Sequence 141696, A
44	11.8	59.0	25	US-11-217-529-171657	Sequence 171657, A
45	11.6	58.0	25	US-11-217-529-6678	Sequence 6678, Ap

# ALIGNMENTS

```

RESULT 1
US-11-217-529-13735/C
Sequence 13735, Application US/11217529
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHITIRO
APPLICANT: NAKAMURA, NORIHIISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 13735
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-13735

Query Match      71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1 AATGAGCCACAGTGTCCA 19
Db      24 ACTGAGCCGCGAGTGTCAA 6

RESULT 2
US-11-217-529-44186/C
Sequence 44186, Application US/11217529
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHITIRO
APPLICANT: NAKAMURA, NORIHIISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529

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CURRENT FILING DATE: 2005-09-02  
PRIOR APPLICATION NUMBER: US 10/932,182  
PRIOR FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 44186  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Saccharomyces pastorianus  
US-11-217-529-44186

Query Match 66.0%; Score 13.2; DB 7; Length 25;  
Best Local Similarity 83.3%; Pred. No. 71;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATAGGCACCAAGTCTCC 18  
22 AATGACCAACCAAGCTTC 5

RESULT 3  
US-11-217-529-86968  
Sequence 86968, Application US/11217529  
Publication No. US20060099612A1  
GENERAL INFORMATION:  
APPLICANT: SUNTORY LIMITED  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHISA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: S-38-285  
CURRENT APPLICATION NUMBER: US/11/217,529  
CURRENT FILING DATE: 2005-09-02  
PRIOR APPLICATION NUMBER: US 10/932,182  
PRIOR FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 86968  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Saccharomyces pastorianus  
US-11-217-529-86968

Query Match 66.0%; Score 13.2; DB 7; Length 25;  
Best Local Similarity 83.3%; Pred. No. 71;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATAGGCACCAAGTCTCA 19  
4 ATAGGCACCAAGTCTCA 21

RESULT 4  
US-10-511-937-2733/C  
Sequence 2733, Application US/10511937  
Publication No. US20060088836A1  
GENERAL INFORMATION:  
APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
APPLICANT: Wohlgenuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
APPLICANT: Prentice, James  
APPLICANT: Morille, Macdonald  
APPLICANT: Rosenberg, Steven  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
FILE REFERENCE: 506612000104  
CURRENT APPLICATION NUMBER: US/10/511,937  
CURRENT FILING DATE: 2004-10-19  
PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR FILING DATE: 2003-04-24  
PRIOR APPLICATION NUMBER: US 10/131,831  
PRIOR FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: US 10/325,899  
PRIOR FILING DATE: 2002-12-20  
NUMBER OF SEQ ID NOS: 3117  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2733  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-511-937-2733

Query Match 66.0%; Score 13.2; DB 6; Length 50;  
Best Local Similarity 83.3%; Pred. No. 82;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGAGCCACCAAGTCTCA 20  
22 TGAACCAACCAAGTCTCA 5

RESULT 5  
US-11-217-529-74193/C  
Sequence 74193, Application US/11217529  
Publication No. US20060099612A1  
GENERAL INFORMATION:  
APPLICANT: SUNTORY LIMITED  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHISA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: S-38-285  
CURRENT APPLICATION NUMBER: US/11/217,529  
CURRENT FILING DATE: 2005-09-02  
PRIOR APPLICATION NUMBER: US 10/932,182  
PRIOR FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 74193  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Saccharomyces pastorianus  
US-11-217-529-74193

Query Match 65.0%; Score 13; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATAGGCACCAAGT 14  
22 ATAGGCACCAAGT 10

RESULT 6  
US-11-217-529-88752/C  
Sequence 88752, Application US/11217529  
Publication No. US20060099612A1  
GENERAL INFORMATION:  
APPLICANT: SUNTORY LIMITED  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHISA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: S-38-285  
CURRENT APPLICATION NUMBER: US/11/217,529  
CURRENT FILING DATE: 2005-09-02  
PRIOR APPLICATION NUMBER: US 10/932,182  
PRIOR FILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 88752  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Saccharomyces pastorianus  
US-11-217-529-88752

Query Match 65.0%; Score 13; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCCACCAG 13  
DB 18 AATGAGCCACCAG 6

RESULT 7  
US-11-217-529-9748  
Sequence 9748, Application US/11217529  
Publication No. US20060099612A1  
GENERAL INFORMATION:  
APPLICANT: SUNTORY LIMITED  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHISA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: S-38-285  
CURRENT APPLICATION NUMBER: US/11/217,529  
CURRENT FILING DATE: 2005-09-02  
PRIOR APPLICATION NUMBER: US 10/932,182  
PRIOR FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 9748  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Saccharomyces pastorianus  
US-11-217-529-9748

Query Match 64.0%; Score 12.8; DB 7; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGCCACCACTGTCCA 19  
DB 7 GAGCCATCAGGCTCCA 22

RESULT 8  
US-11-217-529-117069  
Sequence 117069, Application US/11217529  
Publication No. US20060099612A1  
GENERAL INFORMATION:  
APPLICANT: SUNTORY LIMITED  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHISA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: S-38-285  
CURRENT APPLICATION NUMBER: US/11/217,529  
CURRENT FILING DATE: 2005-09-02  
PRIOR APPLICATION NUMBER: US 10/932,182  
PRIOR FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 117069  
LENGTH: 25  
TYPE: DNA

ORGANISM: Saccharomyces pastorianus  
US-11-217-529-117069

Query Match 64.0%; Score 12.8; DB 7; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATGAGCCACCACTGTCTC 17  
DB 6 ATGAGCCACCACTGTCTC 21

RESULT 9  
US-11-217-529-22469  
Sequence 22469, Application US/11217529  
Publication No. US20060099612A1  
GENERAL INFORMATION:  
APPLICANT: SUNTORY LIMITED  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHISA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: S-38-285  
CURRENT APPLICATION NUMBER: US/11/217,529  
CURRENT FILING DATE: 2005-09-02  
PRIOR APPLICATION NUMBER: US 10/932,182  
PRIOR FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 22469  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Saccharomyces pastorianus  
US-11-217-529-22469

Query Match 63.0%; Score 12.6; DB 7; Length 25;  
Best Local Similarity 78.9%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATGAGCCACCACTGTCCAA 20  
DB 4 AAGAGCCACCTTGCCCAA 22

RESULT 10  
US-11-217-529-71644/c  
Sequence 71644, Application US/11217529  
Publication No. US20060099612A1  
GENERAL INFORMATION:  
APPLICANT: SUNTORY LIMITED  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHISA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: S-38-285  
CURRENT APPLICATION NUMBER: US/11/217,529  
CURRENT FILING DATE: 2005-09-02  
PRIOR APPLICATION NUMBER: US 10/932,182  
PRIOR FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 71644  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Saccharomyces pastorianus  
US-11-217-529-71644

Query Match 63.0%; Score 12.6; DB 7; Length 25;  
Best Local Similarity 78.9%; Pred. No. 1.5e+02;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCA 19

DB 24 AAGAGCCACCACTGTGTACA 6

## RESULT 11

US-11-217-529-125526  
; Sequence 125526, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 125526  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-125526

Query Match 63.0%; Score 12.6; DB 7; Length 25;

Best Local Similarity 78.9%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCA 19

DB 1 AATGAGCCACCACTGTGTACA 19

## RESULT 12

US-11-217-529-8089/c  
; Sequence 8089, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 8089  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-8089

Query Match 62.0%; Score 12.4; DB 7; Length 25;

Best Local Similarity 92.9%; Pred. No. 1.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGCCACCACTGTTC 17

DB 18 GAGCCACCACTGTTC 5

RESULT 13  
US-11-217-529-45366  
; Sequence 45366, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 45366  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-45366

Query Match 62.0%; Score 12.4; DB 7; Length 25;

Best Local Similarity 92.9%; Pred. No. 1.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCACCACTGTCCA 20

DB 7 CCACCACTGTCCA 20

## RESULT 14

US-11-217-529-29471/c  
; Sequence 29471, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 29471  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-29471

Query Match 61.0%; Score 12.2; DB 7; Length 25;

Best Local Similarity 82.4%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GAGCCACCACTGTCCA 20

DB 21 GAGCCACCACTGTCCA 5

## RESULT 15

US-11-217-529-38860/c  
; Sequence 38860, Application US/11217529



```

; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIYO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38860
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-38860
    
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```

Query Match      61.0%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred.No.2.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      4 GAGCCACGAGTGTCCAA 20
      ||| ||||| |||
Db      21 GAGTACCGAGTGTACAA 5
    
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Search completed: May 21, 2006, 22:34:13  
 Job time : 32.5 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:09:23 ; Search time 1331 Seconds  
(without alignments)  
960.893 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagccaccagtcgtccaa 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

GenBml:\*  
1: gb\_env:\*  
2: gb\_pac:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vl:\*  
11: gb\_ov:\*  
12: gb\_hcg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	20	100.0	492	7	G72559	G72559 MARC 6691-6
C 2	20	100.0	928	7	G72558	G72558 MARC 6693-6
C 3	20	100.0	1252	5	HSTUNRA	X72726 H. sapiens t
C 4	20	100.0	3013	14	AY971808	AY971808 Pantholop
C 5	20	100.0	3217	6	DQ229099	DQ229099 Bos grunni
C 6	20	100.0	3296	14	AY621118	AY621118 Bos grunni
C 7	20	100.0	3669	5	AB169332	AB169332 Macaca fa
C 8	20	100.0	188107	5	CN801DME	AL137129 Human chr
C 9	20	100.0	248982	12	AC156150	AC156150 Bos tauru
C 10	18.4	92.0	311	2	AX986444	AX986444 Sequence
C 11	18.4	92.0	311	2	BD121303	BD121303 EST and e
C 12	18.4	92.0	311	2	AR425750	AR425750 Sequence
C 13	18.4	92.0	375	2	CO696751	CO696751 Sequence
C 14	18.4	92.0	1172	7	G26793	G26793 human STS S
C 15	18.4	92.0	1558	5	HSHIF1A13	AF050127 Homo sapi
C 16	18.4	92.0	2537	5	AF207602	AF207602 Homo sapi
C 17	18.4	92.0	2711	6	RNHYPAC1	Y09507 R. norvegicu
C 18	18.4	92.0	3229	2	ARS31606	ARS31606 Sequence

C 19	18.4	92.0	3551	5	AB073325	AB073325 Homo sapi
C 20	18.4	92.0	3678	2	AR642334	AR642334 Sequence
C 21	18.4	92.0	3678	2	AX504300	AX504300 Sequence
C 22	18.4	92.0	3678	2	AX770508	AX770508 Sequence
C 23	18.4	92.0	3678	2	HSU22431	HSU22431 Human hypox
C 24	18.4	92.0	3736	5	BD222980	BD222980 Stable hy
C 25	18.4	92.0	3736	2	AR317244	AR317244 Sequence
C 26	18.4	92.0	3927	2	CO719027	CO719027 Sequence
C 27	18.4	92.0	3927	2	AX321214	AX321214 Sequence
C 28	18.4	92.0	3933	2	AX763546	AX763546 Sequence
C 29	18.4	92.0	3933	5	BC012527	BC012527 Homo sapi
C 30	18.4	92.0	3933	5	HSU29165	HSU29165 Human MOP1
C 31	18.4	92.0	3945	5	HSMA08946	HSMA08946 Homo sapi
C 32	18.4	92.0	3958	2	CS097358	CS097358 Sequence
C 33	18.4	92.0	231045	12	AC118105	AC118105 Rattus no
C 34	18.4	92.0	284456	12	AC174572	AC174572 Bos tauru
C 35	18.4	92.0	298281	12	AC174569	AC174569 Bos tauru
C 36	18.4	92.0	450	7	BV003723	BV003723 Sus scrofa
C 37	18	90.0	1321	6	AF006789S15	AF006789 Sus muscu
C 38	18	90.0	3392	6	DQ010149	DQ010149 Microtus
C 39	18	90.0	3718	2	AX694334	AX694334 Sequence
C 40	18	90.0	3718	6	AF057308	AF057308 Rattus no
C 41	18	90.0	3746	2	AX306008	AX306008 Sequence
C 42	18	90.0	3746	6	HSHIF1A1P	X95580 M. musculus
C 43	18	90.0	3867	6	MMU59496	MMU59496 M. musculus
C 44	18	90.0	3973	6	AF003695	AF003695 Mus muscu
C 45	18	90.0	3973	6	AF003695	AF003695 Mus muscu

#### ALIGNMENTS

RESULT 1  
G72559/c  
LOCUS MARC 6691-6694:992007331.1 SCF - porcine spleen Sus scrofa STS  
DEFINITION genomic, sequence tagged site.  
ACCESSION G72559  
VERSION G72559.1 GI:15146589  
KEYWORDS STS.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Mammalia; Eutheria; laurasiatheria; Cetartiodactyla; Suidae; Suidae;  
Sus 1 (bases 1 to 492)  
Fahnenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L. and  
Keeler, J.W.  
Single nucleotide polymorphism (SNP) discovery in expressed porcine  
genes  
Unpublished (2001)

#### JOURNAL COMMENT

Contact: Freking BA  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4278  
Fax: 402 762 4173  
Email: freking@ma.ars.usda.gov  
Primer A: TACGAGCAGCAGAACTCTAC  
Primer B: TGTGCAATGTGCTACTC  
STS size: 520  
PCR Profile:  
Hotstart: 95 degrees for 15 minutes  
Denature: 95 degrees for 30 seconds  
Anneal: 58 degrees  
Extension: 68 degrees for 2 minutes  
Cycles: 32 to 45  
Protocol:  
Template: 50-200 ng genomic DNA  
Primer: each 20 pmol  
dNTPs: each 88 uM  
Tag Polymerase: 0.25 units (Qiagen HotStar)

Buffer:  
Commercially supplied Qiagen HotStar buffer

The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of 20 or greater. Amplicon size was estimated by agarose gel electrophoresis.

#### FEATURES

source

Location/Qualifiers

1..492  
/organism="Sus scrofa"  
/mol\_type="genomic DNA"  
/strain="white composite, duroc, meishan, minzhu, fengjing, crossbreds"  
/db\_xref="taxon:9823"  
/sex="male and female"  
/clone\_lib="SCF - porcine spleen"  
/dev\_stage="adult"  
/note="Organ: spleen"  
<1..>492

#### ORIGIN

STS

Query Match 100.0%; Score 20; DB 7; Length 492;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACGAGTGTCCAA 20  
|||||  
94 AATGAGCCACGAGTGTCCAA 75

#### RESULT 2

G72558/c

LOCUS

DEFINITION

ACCESION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4278

Fax: 402 762 4173

Email: freking@mail.marc.usda.gov

Primer A: TGTGAGTTATGCTCTATA

Primer B: AAAAGAGTTTATATAGGAC

STS size: 560

PCR Profile:

Hotstart: 95 degrees for 15 minutes

Denature: 95 degrees for 30 seconds

Anneal: 58 degrees

Extension: 68 degrees for 2 minutes

Cycles: 32 to 45

Protocol:

Template: 50-200 ng genomic DNA

Primer: each 20 pmols

dNTPs: each 88 uM

Tag Polymerase: 0.25 units (Qiagen HotStar)

Buffer:  
Commercially supplied Qiagen HotStar buffer

The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of 20 or greater. Amplicon size was estimated by agarose gel electrophoresis.

#### FEATURES

source

Location/Qualifiers

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/mol\_type="genomic DNA"  
/strain="white composite, duroc, meishan, minzhu, fengjing, crossbreds"  
/db\_xref="taxon:9823"  
/sex="male and female"  
/clone\_lib="SCF - porcine spleen"  
/dev\_stage="adult"  
/note="Organ: spleen"  
<1..>928

#### ORIGIN

STS

Query Match 100.0%; Score 20; DB 7; Length 928;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACGAGTGTCCAA 20  
|||||  
57 AATGAGCCACGAGTGTCCAA 38

#### RESULT 3

HSTNPA/c

LOCUS

DEFINITION

ACCESION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

PUBLISHED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..1252  
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/mol\_type="mRNA"  
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/chromosome="9"  
/clone="KL, A"  
/cell\_line="AMA cells"



KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Bos grunniens (domestic yak)  
Bos grunniens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 3296)  
Dolt, K.S. and Qader Pasha, M.A.  
Direct Submission  
Submitted (10-May-2004) Functional Genomics Unit, Institute of  
Genomics and Integrative Biology, Mall Road, Delhi 110007, India  
Location/Qualifiers  
1. .3296  
/organism="Bos grunniens"  
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2. .2473  
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QNTORSFLRMKCTLTSGRTNWKISATWVKLHCTGHIVYDINSQSCGKVPMT  
CVLICEPIPHSNIEIPLDSKTFLSRLDMKFSYCDERITELMGVEBELGRSY  
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EPDALLAPAAAGDTTISLDRGSDPTDQCEEPVLYNDVLPSSNRKLQNTILAM  
SPPASSTKPCSSADPALNDVALKLPNPESLSTMPQIQQPASPDGSTRQ  
SSPPSPSEPCSDVDSDVNEFKELVKEFLPADTEAKNPSTQTDLDLELAVY  
PMDDPQLRSFPLQSLPENSSTSPQASNTVQPYOMQEPPIATVTTATDELTAV  
TQGMEDIKILAFSPHPVKEPPCATSPYSDGSTRASPRAGKVIETORKEHP  
RSPNVLVALSRTQTPEREINPKILQNAQRKRIEHDGSLFOAVGIGTLLQCPD  
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2474. .3296  
/gene="HIF-1A"

ORIGIN  
3'UTR

Query Match 100.0%; Score 20; DB 14; Length 3296;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACAGTGTCCAA 20  
|||||  
DB 2519 AATGAGCCACAGTGTCCAA 2500

RESULT 7  
ABI69332/c  
LOCUS  
DEFINITION  
AB169332 3669 bp mRNA linear pri 17-SEP-2005  
Macaca fascicularis testis cDNA, clone: QCSA-19088, similar to  
human hypoxia-inducible factor 1, alpha subunit  
(basic helix-loop-helix transcription factor) (HIF1A), transcript  
variant 1, mRNA, RefSeq: NM\_001530.2.  
ACCESSION  
ABI69332  
ABI69332.1 GI:67970145  
oligo capping; f1a (full insert sequence).  
KEYWORDS  
Macaca fascicularis (crab-eating macaque).  
SOURCE  
Macaca fascicularis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Cercopithecoidea; Cercopithecinae; Macaca.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Osada, N., Hirata, M., Tanuma, R., Kusuda, J., Hida, M., Suzuki, Y.,  
Sugano, S., Gotohori, T., Shen, C.-K.J., Wu, C.I. and Hashimoto, K.  
Substitution Rate and Structural Divergence of 5'UTR Evolution:  
Comparative Analysis Between Human and Cynomolgus Monkey cDNAs

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
CONSRTM  
TITLE  
JOURNAL  
AUTHORS  
TITLE  
JOURNAL

Mol. Biol. Evol. 22 (10), 1976-1992 (2005)  
15944441  
2  
International consortium for macaque cDNA sequencing and analysis  
DNA sequences of macaque genes expressed in brain or testis and its  
evolutionary implications  
Unpublished  
3 (bases 1 to 3669)  
Hashimoto, K., Kusuda, J. and Sugano, S.  
Direct Submission  
Submitted (18-MAR-2004) Katsuyuki Hashimoto, National Institute of  
Infectious Diseases, Division of Genetic Resources, 23-1, Toyama  
1-chome, Shinjuku-ku, Tokyo, 162-8640, Japan  
(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,  
Tel: 81-3-5285-1111 (ex.2120), Fax: 81-3-5285-1181)  
The international consortium for macaque cDNA sequencing and  
analysis consists of: Department of Virology and Human Genome  
Center, Institute of Medical Science, The University of Tokyo,  
Tokyo, Japan; Division of Genetic Resources, National Institute of  
Infectious Diseases of Japan, Tokyo, Japan; National Health  
Research Institute, Taipei, Taiwan; Institute of Molecular Biology,  
Academia Sinica, Taipei, Taiwan; Department of Ecology & Evolution,  
University of Chicago, Chicago, IL, USA; Center for Information  
Biology, National Institute of Genetics of Japan, Mishima, Japan.  
Clone distribution: clone distribution information can be found at:  
http://www.nih.go.jp/yoken/genebank/  
lab host: TOP10  
Vector: pME18S-FL3 (Acc.No. AB009864)  
R. Site1: DraIII (CACTGCTG)  
R. Site2: DraIII (CAGCAGTG)  
Description: 1st strand cDNA was primed with an oligo(dT) primer  
(ATGCGCTTTTCTTTTCTTTT), double-stranded cDNA was synthesized  
using specific 5' and 3' primers and amplified by PCR. The PCR  
product was digested with SfiI and size selection was performed to  
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned  
into distinct DraIII sites of pME18S-FL3. XhoI sites just outside  
the DraIII sites can be used to isolate the cDNA insert. Libraries  
were constructed by oligo-capping method. Libraries were made from:  
QCSA: cerebellum cortex  
QNSA: parietal lobe  
QTRA: temporal lobe right  
QFLA: frontal lobe left  
QMSA: medulla oblongata  
QBSA: brain stem  
QORA: occipital lobe right  
QCSA: testis  
Custom primers were used for 5' and 3'-end sequencing. The  
full-insert sequencing was done by primer-walking method using ABI  
DNA sequencer.  
Location/Qualifiers  
1. .3669  
/organism="Macaca fascicularis"  
/mol\_type="mRNA"  
/db\_xref="taxon:9541"  
/clone="QCSA-19088"  
/sex="male"  
/clone\_lib="macaque cDNA library QCSA"  
/dev\_stage="adult"  
297. .2777  
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(basic helix-loop-helix transcription factor)  
(HIF1A), transcript variant 1, mRNA, RefSeq: NM\_001530.2"  
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/protein\_id="BAB01417.1"  
/db\_xref="GI:67970146"  
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QNTORSFLRMKCTLTSGRTNWKISATWVKLHCTGHIVYDINSQSCGKVPMT  
CVLICEPIPHSNIEIPLDSKTFLSRLDMKFSYCDERITELMGVEBELGRSY  
EYHALSDHILTKTHHGMFTKGYVTRMLAKRGVYVWIEQAVIYNTNSQPC

IVCVNYVSGIIQHDLIFSLQTECVLKPVESSDMKXTOLFTKVESDTSLSLPDKLK  
 BPDALTLIAPAGDTIISLDGNSDITDQLEBPLVNDVMI.PSSNEKQNTNLM  
 SPLESTPKPLSADPALQEVALKLEPPELSLFTMPQLODDPSPDSSTG  
 SSEPSNPSXCFYVDSMDVNBFLGLVEVKEFLADTAKNPFSDDDLEMLAPYI  
 PMDDPOLRSFOLSPLESSASPESSATOSTVTPQTOIQEPTANATTTATYDEL  
 KYTKKDMEDIKILIASPSTHHTKTSKTSSTYRTQSTKASPNAGKGVLEQTK  
 SHRSFVNLSTVSTQRTTVEEINPILALQNAQRKMEHDSLFQAVIGITLQO  
 PDDHAATSLSMKRVKCKSKSEKNGMEKTIILIPDLACRLLAQSDMSGLPOLTSY  
 DCEVNAPIQSRNLAGEBILRALDQVN"

## ORIGIN

Query Match 100.0%; Score 20; DB 5; Length 3669;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACAGTGTCCAA 20  
 Db 2823 AATGAGCCACAGTGTCCAA 2804

RESULT 8  
 CNS01DWE/c 188107 bp DNA linear PRI 30-APR-2001  
 LOCUS Human chromosome 14 DNA sequence BAC R-618G20 of library RPCI-11  
 DEFINITION from chromosome 14 of Homo sapiens (Human), complete sequence.  
 ACCESSION AL137129  
 VERSION AL137129.4 GI:13928034  
 KEYWORDS HTG.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.

1 (bases 1 to 188107)  
 Heilig, R., Pettit, J.L., Vico, V., Dasilva, C., Robert, C., Winkler, P.,  
 Brothier, P., Catolico, L., Barbe, V., Pelletier, B., Artiguenave, F.,  
 Levy, M., Eckenberg, R., Brula, T., deBardine, V., Crnaud, C.,  
 Gyapay, G., Saurin, W. and Weissenbach, J.  
 Sequencing of the human chromosome 14  
 Unpublished  
 2 (bases 1 to 188107)  
 Genoscope.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 JOURNAL

COMMENT Direct Submission  
 Submitted (30-APR-2001) Genoscope - Centre National de Sequencage :  
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 On May 2, 2001 this sequence version replaced gi:12580637.  
 Web : www.genoscope.cns.fr  
 Center: Genoscope / Centre National de Sequencage  
 Center code: GS  
 Web site: http://www.genoscope.cns.fr/  
 Contact: SeqRef@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.  
 Upstream BAC (overlapping the T7 end) : R-47122  
 Downstream BAC (overlapping the SP6 end) : R-442G21 (AC-AL137918)  
 Assembly program: Phrap, version 2.0  
 Quality coverage: 7.05x in Q20 bases; sum-of-contigs

## Range all quality chart :

0 - 9 : 10  
 10 - 19 : 85  
 20 - 29 : 198  
 30 - 39 : 610  
 40 - 49 : 3583  
 50 - 59 : 6533  
 60 - 69 : 7937  
 70 - 79 : 18709  
 80 - 89 : 53590

90 - 99 : 96831  
 -----  
 Percentage of bases with a quality value >= 40 : 99 %  
 Location/Qualifiers

## FEATURES

## Source

## STS

Identified using the e-PCR software (G. Schuler)"  
 169977..170107  
 /note="matching EMBL:G14590  
 Rdb:RH7938  
 dbSTS:STS30175

## STS

Identified using the e-PCR software (G. Schuler)"  
 184217..184356  
 /note="matching EMBL:U44754  
 Rdb:RH75870  
 dbSTS:STS52358

## STS

Identified using the e-PCR software (G. Schuler)"  
 184629..184708  
 /note="matching EMBL:AA496975  
 Rdb:RH93275  
 dbSTS:STS66278

## STS

## ORIGIN

Query Match 100.0%; Score 20; DB 5; Length 188107;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACAGTGTCCAA 20  
 Db 136374 AATGAGCCACAGTGTCCAA 136355

RESULT 9  
 AC156150 248982 bp DNA linear HTG 01-JUL-2005  
 LOCUS Bos taurus clone CH240-47113, \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 DEFINITION unordered pieces.  
 AC156150  
 AC156150.2 GI:68265447  
 HTG, HTGS\_PHASE1, HTGS\_DRAFT, HTGS\_ENRICHED.  
 KEYWORDS Bos taurus (cattle)  
 SOURCE Bos taurus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 248982)  
 Muzny, D., Martie, Metzker, M., Lee, A., Abramson, S., Adams, C., Alder, J.,  
 Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D.,  
 Anyalebech, V., Ayogel, A., Ayodeji, M., Baca, B., Baden, H.,  
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benhmed, F.,  
 Biewald, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,  
 Bryant, N., Bunay, C., Burch, P., Butrell, K., Calderon, B.,  
 Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,  
 Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,  
 Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,  
 Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,  
 Delgado, O., Denson, S., Derramo, C., Ding, Y., Dinh, H., Divya, K.,  
 Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,  
 Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,  
 Fernandez, S., Finley, M., Flagg, R., Forbes, L., Foster, M., Foster, P.,  
 Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,  
 Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,  
 Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,

Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogue, M., Hollins, B., Howells, S., Hu, Y., Hume, J., Idol, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kover, C., Kowalski, C., Kraft, C.L., Ledow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenz, L., Loussier, H., Lozada, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., Manthey, S., McLeod, M.P., McNeill, T.Z., Meenan, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, S., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackel, O., Okunuga, G., Olamunsgoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Plankoch, C., Plopper, P., Polindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Saverly, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smales, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K., Valas, R., Vera, V., Villaseca, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wood, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

## Direct Submission

Unpublished

2 (bases 1 to 248982)

Worley, K.C.

## Direct Submission

Submitted (25-JAN-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 248982)

## Cow Genome Sequencing Consortium.

## Direct Submission

Submitted (01-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

## COMMENT

## REFERENCE

## JOURNAL

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gap 164002..164051  
/estimated\_length=50  
gap 226342..226391  
/estimated\_length=50  
gap 230590..230639  
/estimated\_length=50  
gap 235990..236089  
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gap 245461..245560  
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gap 246565..246664  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 79;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20  
Db 187060 AATGAGCCACCAAGTGTCCAA 187079

RESULT 10  
LOCUS AX986444 311 bp DNA  
DEFINITION Sequence 17247 from Patent EP1104808.  
ACCESSION AX986444  
VERSION AX986444.1 GI:4092584  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1  
Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.  
ESTs and encoded human proteins  
Patent: EP 1104808-A 17247 06-JUN-2001;  
Genet (FR)  
Location/Qualifiers  
1..311  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
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FEATURES  
source

ORIGIN  
Query Match 92.0%; Score 18.4; DB 2; Length 311;  
Best Local Similarity 95.0%; Pred. No. 1.8e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20  
Db 198 AGTGAGCCACCAAGTGTCCAA 179

RESULT 11  
BD121303/c 311 bp DNA linear PAT 18-SEP-2002  
LOCUS BD121303  
DEFINITION EST and encoded human protein.  
ACCESSION BD121303  
VERSION BD121303.1 GI:23216213  
KEYWORDS JP 2002010789-A/13380.  
SOURCE Homo sapiens (human)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE Homidae; Homo.  
AUTHORS 1 (bases 1 to 311)  
TITLES Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.  
JOURNAL EST and encoded human protein  
Patent: JP 2002010789-A 13380 15-JAN-2002;  
GENSET CORP  
COMMENT  
OS Homo sapiens (human)  
PN JP 2002010789-A/13380  
PD 15-JAN-2002  
PF 07-AUG-2000 JP 2000280989  
PR 05-AUG-1999 US 60/147499  
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE  
GIORDANO  
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC  
C12N1/21, PC  
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC  
C12N15/00  
CC EST and encoded human protein  
FH Key Location/Qualifiers  
FT source 1..311  
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Location/Qualifiers  
1..311  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

FEATURES  
source

ORIGIN  
Query Match 92.0%; Score 18.4; DB 2; Length 311;  
Best Local Similarity 95.0%; Pred. No. 1.8e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20  
Db 198 AGTGAGCCACCAAGTGTCCAA 179

RESULT 12  
AR425750/c 311 bp DNA linear PAT 18-DEC-2003  
LOCUS AR425750  
DEFINITION Sequence 17247 from patent US 6639063.  
ACCESSION AR425750  
VERSION AR425750.1 GI:40180660  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 311)  
TITLES Edwards, J.B.D.M., Jobert, S. and Giordano, J.-Y.  
JOURNAL EST's and encoded human proteins  
Patent: US 6639063-A 17247 28-OCT-2003;  
Genet S.A. !  
WOX;  
Location/Qualifiers  
1..311  
/organism="unknown"  
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FEATURES  
source

ORIGIN  
Query Match 92.0%; Score 18.4; DB 2; Length 311;  
Best Local Similarity 95.0%; Pred. No. 1.8e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20  
Db 198 AGTGAGCCACCAAGTGTCCAA 179

RESULT 13  
C0696751/c 375 bp DNA linear PAT 03-FEB-2004  
LOCUS C0696751  
DEFINITION Sequence 41677 from Patent WO02070737.  
ACCESSION C0696751



VERSION C0696751.1 GI:42246561  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
REFERENCE  
AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.  
TITLE Compositions and methods relating to osteoarthritis  
JOURNAL Patent: WO 0207037-A 41677 12-Sep-2002;  
Chondrogene Inc. (CA)  
FEATURES  
source location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 92.0%; Score 18.4; DB 2; Length 375;  
Best Local Similarity 95.0%; Pred. No. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AATGAGCCACCACTGTCCAA 20  
1 1172 bp DNA linear STS 02-JUN-1996  
Db 165 AGTGAAGCCACCACTGTCCAA 146  
RESULT 14  
G26793/c 1172 bp DNA linear STS 02-JUN-1996  
LOCUS human STS\_U22431, sequence tagged site.  
DEFINITION G26793  
ACCESSION G26793  
VERSION G26793.1 GI:1349025  
KEYWORDS STS; STS sequence; primer; sequence tagged site.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
REFERENCE  
AUTHORS Hudson, T.  
TITLE Whitehead Institute/MIT Center for Genome Research; Physically  
JOURNAL Mapped STS  
COMMENT Unpublished (1995)  
Contact: Thomas Hudson  
Whitehead Institute/MIT Center for Genome Research  
9 Cambridge Center, Cambridge MA 02142 USA  
Tel: 617 252 1900  
Fax: 617 252 1902  
Email: thudson@genome.wi.mit.edu  
Primer A: TGGACACTGTGGCTCACTA  
Primer B: ATGCTACTGCATGCAATG  
STS size: 223  
PCR Profile:  
Presoak:  
Denaturation:  
Annealing: 56 degrees C  
Polymerization:  
PCR Cycles: 35  
Thermal Cycler:  
Protocol:  
Template: 10 ng  
Primer: each 5 pM  
dNTPs: each 4 mM  
Tag Polymerase: 0.025 units/ul  
Total Vol: 20 ul  
Buffer:  
MgCl2: 1.5 mM

KCl: 50 mM  
Tris-HCl: 10 mM  
pH: 9.3  
FEATURES  
source Derived from dbEST (Genbank accession U22431).  
location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/map="211.5 CR from top of Chr14 linkage group"  
STS 31..253  
primer\_bind 31..50  
primer\_bind complement(234..253)  
ORIGIN  
Query Match 92.0%; Score 18.4; DB 7; Length 1172;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AATGAGCCACCACTGTCCAA 20  
1 1172 bp DNA linear PRI 26-OCT-1998  
Db 49 AGTGAAGCCACCACTGTCCAA 30  
RESULT 15  
HSH1F1A13/c 1558 bp DNA linear PRI 26-OCT-1998  
LOCUS Homo sapiens hypoxia-inducible factor 1 alpha subunit (HIF1A) gene,  
DEFINITION exon 15 and complete cds.  
ACCESSION AF050127  
VERSION AF050127.1 GI:3790533  
KEYWORDS 13 of 13  
SEGMENT Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
REFERENCE  
AUTHORS Iyer, N.V., Leung, S.W. and Semenza, G.L.  
TITLE The human hypoxia-inducible factor 1alpha gene: HIF1A structure and  
JOURNAL evolutionary conservation  
PUBMED Genomics 52 (2), 159-165 (1998)  
9782081  
REFERENCES  
AUTHORS 2 (bases 1 to 1558)  
TITLE Iyer, N.V., Leung, S.W. and Semenza, G.L.  
JOURNAL Direct Submision  
COMMENT Submitted (24-FEB-1998) Department of Pediatrics and Medicine,  
Institute of Genetic Medicine, Johns Hopkins University School of  
Medicine, 600 N. Wolfe St, Baltimore, MD 21287-3914, USA  
FEATURES  
source location/Qualifiers  
1..1558  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="14"  
/map="14q21-q24"  
order(AF050115..1:1..1066,AF050116..1:1..441,  
AF050117..1:1..538,AF050118..1:1..423,AF050119..1:1..352,  
AF050120..1:1..251,AF050121..1:1..422,AF050122..1:1..576,  
AF050123..1:1..527,AF050124..1:1..996,AF050125..1:1..551,  
AF050126..1:1..392,1..1413)  
/gene="HIF1A"  
join(AF050115..1:642..960,AF050116..1:177..367,  
AF050117..1:68..213,AF050118..1:298..382,  
AF050119..1:174..286,AF050120..1:188..408,  
AF050121..1:134..281,AF050122..1:1219..341,  
AF050123..1:120..406,AF050124..1:219..341,  
AF050125..1:184..292,  
AF050126..1:138..264,93..1413)  
/gene="HIF1A"  
/product="hypoxia-inducible factor 1 alpha subunit"

CDS

join(AF050115.1:926..960,AF050116.1:177..367,  
AF050117.1:68..213,AF050117.1:298..382,  
AF050118.1:174..286,AF050119.1:58..260,AF050120.1:84..190,  
AF050121.1:134..281,AF050122.1:188..408,  
AF050123.1:120..406,AF050124.1:219..341,  
AF050124.1:469..902,AF050125.1:184..292,  
AF050126.1:138..264,93..244)  
/gene="HIF1A"

/codon\_start=1

/product="hypoxia-inducible factor 1 alpha subunit"

/protein\_id="AAC8568.1"

/db\_xref="GI:3790535"

/translation="MEGAGGANDKKKISSRRRKKSRDAARSRRSKSEVFEYELAQGL  
PLPNVSSHLDKASVWRLLTISYLRRLDAGDLIDEDDKAQNNCFYLKALDGFVAV  
LTDGDWYISDNVNTKMGLTQFELTGHVDFTHPCDHEMRMLTHRGLVYKGS  
QNTORSFPLAMKCTLTSGRTNMTKSAITWYLCGTHIHYDNTSNQPOGYYKKPMT  
CLYLICERPIPHPSNIEIPLDKRTPLSRHSIDMKFSYCDERITELMGTPEBLGRSTY  
EYHALDSHLTKTHDMFTKQVTTQYRLARQGVWVEVTOATVINYTKNSQPQC  
IVCNVYVSGIIOHDLIFSLQTECVAKPVESDMKMTQLFTKVESDTSLPDKLK  
EPDALTLAPAGPTIISLDGSDNTEEDDQLEVPYNDVMLPSNKKLONINLAM  
SPLPATAETPKPLRSADPALNOEVALKLEPNPSLELFTMPQIOTDOTPSPSDSTRO  
SSPEPNSPSEYCFYVSDMNTPEKLELVKELPAEDTEAKNPFSTQDTDLDEMLAPYI  
PMDDUQLRSPDQLSPLESSASPSKASPOSTVTFVFOQTQIQEPTNATTTATTDL  
KTVYKDMEDIKILIASPSPTHIKETTSATSSPYRDTGRTASPNRAGVLEQTEK  
SHRSPNVLSVALSORTVPEEBELNPKILALQNAQRKRKMDHDSLFOAVGIGTLLQ  
PDDHAATTSLSWKVKGSKSEQNGMEOKTIIIPSLACRLGQSWDESGLPQLTSY  
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/gene="HIF1A"

/number=14

93..1413

/gene="HIF1A"

/number=15

245..1413

/gene="HIF1A"

1395..1400

/gene="HIF1A"

inttron

exon

3'UTR

polyA\_signal

ORIGIN

QY 1 AATGAGCACCAAGTCCAA 20

DB 290 AGTGGCCACCACTGCCAA 271

Query Match 92.0%; Score 18.4; DB 5; Length 1558;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: May 21, 2006, 22:18:19  
Job time: 1334 secs

GenCore version 5.1.8  
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OM nucleic - nucleic search, using SW model

Run on: May 21, 2006, 21:08:55 / Search time 259.5 Seconds  
(without alignments)  
537.360 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20  
Sequence: 1 aatgagccaccagtcgca 20

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*  
1: geneseqn1980a:\*  
2: geneseqn1990a:\*  
3: geneseqn2000a:\*  
4: geneseqn2001a:\*  
5: geneseqn2001b:\*  
6: geneseqn2002a:\*  
7: geneseqn2002b:\*  
8: geneseqn2003a:\*  
9: geneseqn2003b:\*  
10: geneseqn2003c:\*  
11: geneseqn2003d:\*  
12: geneseqn2004a:\*  
13: geneseqn2004b:\*  
14: geneseqn2005a:\*  
15: geneseqn2005b:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	13	ADQ88722 Human HIF
2	20	100.0	20	13	ADQ88721 Human HIF
3	20	100.0	20	13	ADQ88721 Human HIF
4	20	100.0	20	13	ADQ88721 Human HIF
5	20	100.0	20	13	ADQ88721 Human HIF
6	20	100.0	20	13	ADQ88721 Human HIF
7	20	100.0	20	13	ADQ88721 Human HIF
8	20	100.0	20	13	ADQ88721 Human HIF
9	20	100.0	20	13	ADQ88721 Human HIF
10	20	100.0	20	13	ADQ88721 Human HIF
11	20	100.0	20	13	ADQ88721 Human HIF
12	20	100.0	20	13	ADQ88721 Human HIF
13	20	100.0	20	13	ADQ88721 Human HIF
14	20	100.0	20	13	ADQ88721 Human HIF
15	20	100.0	20	13	ADQ88721 Human HIF

C 19	18.4	92.0	3678	6	ABK84267
C 20	18.4	92.0	3678	8	ACA89893
C 21	18.4	92.0	3678	10	ABZ83187
C 22	18.4	92.0	3678	14	ABD17984
C 23	18.4	92.0	3736	2	AAT45937
C 24	18.4	92.0	3736	3	AAZ99537
C 25	18.4	92.0	3736	9	ADA18530
C 26	18.4	92.0	3736	14	AEC09680
C 27	18.4	92.0	3812	12	ADO26976
C 28	18.4	92.0	3927	6	AA61690
C 29	18.4	92.0	3933	2	AAK58980
C 30	18.4	92.0	3933	8	ADA03184
C 31	18.4	92.0	3933	10	ADD18957
C 32	18.4	92.0	3933	10	ADP30301
C 33	18.4	92.0	3933	10	ADG89361
C 34	18.4	92.0	3933	10	AAI56898
C 35	18.4	92.0	3933	12	ADL83133
C 36	18.4	92.0	3933	12	ADN74936
C 37	18.4	92.0	3933	13	ADR24764
C 38	18.4	92.0	3933	13	ACN39703
C 39	18.4	92.0	3933	13	ADP54154
C 40	18.4	92.0	3933	13	ADT78563
C 41	18.4	92.0	3933	13	ADT78563
C 42	18.4	92.0	3933	13	ADT78563
C 43	18.4	92.0	3938	14	ADX97785
C 44	18.4	92.0	3958	12	ADO26975
C 45	18.4	92.0	3958	14	ADZ36287

ALIGNMENTS

RESULT 1	ADQ88722	standard; DNA; 20 BP.
ID	ADQ88722	
AC	ADQ88722	
DT	21-OCT-2004	(first entry)
DE	Human HIF-1 antisense oligonucleotide RX-0047.	
KW	RX-0047, RX-0149, human, hypoxia inducible factor; HIF-1; cytotoxicity; cancer; infection; inflammation; tumour formation; ss;	
OS	Homo sapiens.	
PN	US2004152655-A1.	
PD	05-AUG-2004.	
PF	28-JAN-2004; 2004US-00766185.	
PR	31-JAN-2003; 2003US-0444367P.	
PA	(YOUNG) YOUNG H.	
PA	(MAO) MAO L.	
PA	(LERY) LERY Y. B.	
PA	(AHNC) AHN C.	
PA	(JIAN) JIANG X.	
PI	Yoon H, Mao L, Lee YB, Ahn C, Jiang X,	
DR	WPI, 2004-561492/54.	
PT	New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a	
PT	nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),	
PT	useful for inhibiting expression of HIF-1 and inducing cytotoxicity in	
PT	several cancer cells.	
PS	Claim 1, SEQ ID NO 2; 35pp; English.	

CC The invention describes a compound, RX-0047 or RX-0149 targeted to a  
CC nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),  
CC where the oligonucleotide compound inhibits the expression of human HIF-  
CC 1. Also described are: a method of inhibiting the expression HIF-1 in  
CC human cells or tissues; and a method of inducing cytotoxicity in a cancer  
CC cell. Specifically claimed are RX-0047 and RX-0149 compounds having a  
CC fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5'  
CC aatggcaccacgtgtccaa 3' and SEQ ID NO. 4, 5' ggagctacatctccaagtc 3',  
CC respectively). The compounds are useful for inhibiting the expression of  
CC HIF-1 and inducing the cytotoxicity in several cancer cells. The  
CC antisense compounds are also useful for preventing or delaying infection,  
CC inflammation, or tumour formation. This sequence represents a human HIF-1  
CC antisense oligonucleotide.

XX  
SQ Sequence 20 BP, 7 A, 6 C, 4 G, 3 T, 0 U, 0 Other;  
Query Match 100.0%; Score 20; DB 13; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCAA 20  
DB 1 AATGAGCCACCACTGTCCAA 20

RESULT 2  
AD088721/C  
ID AD088721 standard; DNA, 20 BP.  
XX  
AC AD088721;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Human hypoxia inducible factor-1 gene fragment seqid 1.  
XX  
KM RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;  
XX cancer; infection; inflammation; tumour formation; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2004152655-A1.  
XX  
PD 05-AUG-2004.  
XX  
PR 28-JAN-2004; 2004US-00766185.  
XX  
PR 31-JAN-2003; 2003US-0444367P.  
XX  
PA (YOON/) YOON H.  
PA (MAOL/) MAO L.  
PA (LEBY/) LEE Y B.  
PA (AHNC/) AHN C.  
PA (JIAN/) JIANG X.  
XX  
PI Yoon H, Mao L, Lee YB, Ahn C, JIANG X;  
XX  
DR WPI; 2004-561492/54.  
XX  
PT New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a  
PT nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),  
PT useful for inhibiting expression of HIF-1 and inducing cytotoxicity in  
PT several cancer cells.  
XX  
PS Disclosure; SEQ ID NO 1, 35pp; English.  
XX  
CC The invention describes a compound, RX-0047 or RX-0149 targeted to a  
CC nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),  
CC where the oligonucleotide compound inhibits the expression of human HIF-  
CC 1. Also described are: a method of inhibiting the expression HIF-1 in  
CC human cells or tissues; and a method of inducing cytotoxicity in a cancer  
CC cell. Specifically claimed are RX-0047 and RX-0149 compounds having a  
CC fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5'  
CC aatggcaccacgtgtccaa 3' and SEQ ID NO. 4, 5' ggagctacatctccaagtc 3',

CC respectively). The compounds are useful for inhibiting the expression of  
CC HIF-1 and inducing the cytotoxicity in several cancer cells. The  
CC antisense compounds are also useful for preventing or delaying infection,  
CC inflammation, or tumour formation. This sequence represents a site on the  
CC HIF-1 to which antisense oligonucleotides can be targeted in order to  
CC control HIF-1 gene expression.

XX  
SQ Sequence 20 BP, 3 A, 4 C, 6 G, 7 T, 0 U, 0 Other;  
Query Match 100.0%; Score 20; DB 13; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCAA 20  
DB 20 AATGAGCCACCACTGTCCAA 1

RESULT 3  
AAK77781  
ID AAK77781 standard; DNA, 27884 BP.  
XX  
AC AAK77781;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32593.  
XX  
KM Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
XX cytostatic; gene therapy; vaccine; metastasis; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200157182-A2.  
XX  
PD 09-AUG-2001.  
XX  
PR 17-JAN-2001; 2001WO-US001354.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225477P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226688P.  
PR 22-AUG-2000; 2000US-0227182P.

[illegible]

```
XX AC ADT78441;
XX XX 27-JAN-2005 (first entry)
XX DE Human HIF1alpha cDNA sequence #2.
XX XX
XX AC Antisense therapy; human; hypoxia-inducible factor 1 alpha;
XX KM hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
XX KM hyperproliferative disorder; cancer; p53; angiogenic disorder;
XX KM eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
XX KM porosis; atherosclerosis; smooth muscle cell proliferation;
XX KM blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
XX KM ophthalmological; antiinflammatory; respiratory; vasotropic; gene; ss.
XX OS Homo sapiens.
XX PN US2004220393-A1.
XX XX
XX PD 04-NOV-2004.
XX XX
XX PF 21-NOV-2003; 2003US-00719370.
XX XX
XX PR 23-NOV-2002; 2002US-00304126.
XX XX
XX PA (WARD/) WARD D T.
XX PA (DOBI/) DOBI K W.
XX PA (MARC/) MARCUSON E G.
XX PA (FRIE/) FRIER S M.
XX PI Ward DT, Dobie KW, Marcuson EG, Freier SM;
XX DR WPI; 2004-774955/76.
XX XX
XX PT New antisense compound which inhibits the expression of hypoxia-inducible
XX PT factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
XX PT hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX XX
XX PS Example 15; SEQ ID NO 11, 195pp; English.
XX XX
XX CC The present invention relates to antisense compounds targeted to nucleic
XX CC acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
XX CC hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
XX CC comprises an antisense oligonucleotide that specifically hybridises with
XX CC the nucleic acid and inhibits the expression of HIF1alpha and/or
XX CC HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
XX CC The antisense oligonucleotide comprises at least one modified
XX CC internucleoside linkage, preferably a phosphorothioate linkage. It also
XX CC comprises at least one modified sugar moiety, preferably a 2'-O-
XX CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
XX CC comprises at least one modified nucleobase, preferably a 5-
XX CC methylcytosine. The antisense oligonucleotides are useful for the
XX CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,
XX CC preferably a cancer carrying a p53 mutation, or an angiogenic disorder
XX CC that affects the eye. The compound is also useful for treating tumours,
XX CC hyperplasias, pulmonary fibrosis, angiogenesis, porosis,
XX CC atherosclerosis and smooth muscle cell proliferation in the blood vessels
XX CC such as stenosis or restenosis following angioplasty. It is also useful
XX CC in drug discovery and target validation, and can be utilised for
XX CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
XX CC The present sequence represents human HIF1alpha cDNA.
XX XX
XX SO Sequence 57500 BP, 17058 A; 10565 C; 10922 G; 18955 T; 0 U; 0 Other;
```

```
Query Match 100.0%; Score 20; DB 13; Length 57500;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AATGAGCCACCACTGTCCAA 20
DB 54374 AATGAGCCACCACTGTCCAA 54355
```

```
RESULT 5
ADN74943/C
ID ADN74943 standard; DNA; 57501 BP.
XX AC ADN74943;
XX XX
XX DT 12-AUG-2004 (first entry)
XX XX
XX DE Genomic DNA encoding human hypoxia-inducible factor 1 alpha.
XX KM de; gene; human; antisense therapy; hypoxia-inducible factor 1 alpha;
XX KM hyperproliferative disorder.
XX XX
XX OS Homo sapiens.
XX PN US2004101858-A1.
XX XX
XX PD 27-MAY-2004.
XX XX
XX PF 23-NOV-2002; 2002US-00304126.
XX XX
XX PR 23-NOV-2002; 2002US-00304126.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX XX
XX PI Ward DT, Dobie KW;
XX XX
XX DR WPI; 2004-399686/37.
XX XX
XX PT New compounds, particularly oligonucleotides targeted to a nucleic acid
XX PT encoding hypoxia-inducible factor 1 alpha, useful for treating diseases
XX PT associated with hypoxia-inducible factor 1 alpha, e.g. hyperproliferative
XX PT disorders.
XX XX
XX PS Example 15; SEQ ID NO 11; 80pp; English.
XX XX
XX CC The invention relates to antisense oligonucleotides targeted to, and
XX CC which specifically hybridise with, and inhibit expression of, a nucleic
XX CC acid molecule encoding hypoxia-inducible factor 1 alpha. The antisense
XX CC oligonucleotides are useful for treating a disease or condition
XX CC associated with hypoxia-inducible factor 1 alpha, such as a
XX CC hyperproliferative disorder. They are also useful in research and
XX CC diagnostics for modulating the expression of hypoxia-inducible factor 1
XX CC alpha. The present sequence represents genomic DNA encoding human hypoxia
XX CC -inducible factor 1 alpha.
XX XX
XX SO Sequence 57501 BP, 17058 A; 10565 C; 10922 G; 18956 T; 0 U; 0 Other;
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Query Match 100.0%; Score 20; DB 12; Length 57501;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 54375 AATGAGCCACCACTGTCCAA 54356
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```
RESULT 6
AAK78996
ID AAK78996 standard; DNA; 37 BP.
XX AC AAK78996;
XX XX
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```
DT 17-AUG-1999 (first entry)
```

```
DE HIF-1alpha gene amplification primer #2.
```

```
KM Chimeric; transactivator protein; DNA binding domain; HIF; VP16;
KM hypoxia-inducible factor; transcriptional activation; expression vector;
KM normoxic; ischaemic tissue; damage; ss.
```

```
OS Synthetic.
OS Homo sapiens.
```

XX MO9928469-A1.  
 XX 10-JUN-1999.  
 XX  
 XX 04-DEC-1998; 98WO-US025753.  
 XX  
 XX 04-DEC-1997; 97US-0067546P.  
 XX 13-AUG-1998; 98US-00133612.  
 XX  
 XX (GENZ ) GENZYME CORP.  
 XX  
 XX Gregory RJ, Vincent K;  
 XX WPI; 1999-371122/31.  
 XX  
 XX Novel nucleic acid encoding a chimeric transactivator.  
 XX  
 XX Example 1, Page 74; 81pp; English.  
 XX  
 XX The invention relates to a new nucleic acid molecule encoding an active  
 XX chimeric transactivator protein which comprises (i) the DNA binding  
 XX domain of a hypoxia-inducible factor protein; and (ii) a protein domain  
 XX capable of transcriptional activation e.g. the transactivation domain of  
 XX VP16. The expression vector is used to increase, in a target cell, the  
 XX expression of a hypoxia-inducible gene. The vector allows sustained  
 XX expression of active HIF-1a in cells under normoxic conditions and is  
 XX used for reducing ischemic tissue damage in a subject having a hypoxia-  
 XX associated disorder. The primers MAX78995-X78996 were used to PCR amplify  
 XX the full length HIF-1alpha gene for generating the chimeric construct  
 XX  
 XX Sequence 37 BP; 13 A; 8 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 2; Length 37;  
 Best Local Similarity 95.0%; Pred. No. 16;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCAA 20  
 | | | | | | | | | | | | | | | | | | | | | |  
 DB 8 AATGAGCCACCACTGTCCAA 27

RESULT 7  
 ADR12339/c  
 ID ADR12339 standard; DNA; 1192 BP.  
 XX  
 XX ADR12339;  
 XX  
 XX 21-OCT-2004 (first entry)  
 XX  
 XX Human hypoxia-inducible factor a 3'-untranslated region DNA.  
 XX  
 XX 88; cytoskeletal; VEGF modulator; angiogenesis inhibitor;  
 XX UTR-dependent expression; vascular endothelial growth factor;  
 XX untranslated region; cancer; angiogenesis.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO2004065561-A2.  
 XX  
 XX 05-AUG-2004.  
 XX  
 XX 21-JAN-2004; 2004WO-US001643.  
 XX  
 XX 21-JAN-2003; 2003US-0441637P.  
 XX  
 XX (PTCT-) PTC THERAPEUTICS INC.  
 XX  
 XX Cao L, Trifilidis P;  
 XX WPI; 2004-571681/55.  
 XX  
 XX Identifying modulators of untranslated region-dependent expression of a

PT VEGF gene, useful for treating cancer, comprises contacting a compound  
 PT with a cell or translation mixture containing a reporter gene linked to a  
 PT VEGF gene UTR.  
 XX  
 XX Example; SEQ ID NO 48; 251pp; English.  
 XX  
 XX A method of identifying (M1) a compound that modulates untranslated  
 XX region-dependent expression of a vascular endothelial growth factor  
 XX (VEGF) gene comprises contacting a member of a library of compounds with  
 XX a cell or cell-free translation mixture containing a reporter gene  
 XX operably linked to an untranslated region (UTR) of the VEGF gene, and  
 XX detecting expression of the reporter gene. A compound is identified as  
 XX modulator if the level of expression of the reporter gene in the presence  
 XX of the compound is altered as compared to that in the absence of the  
 XX compound or in the presence of a control. Compounds identified by M1 are  
 XX useful for treating, preventing or ameliorating cancer or its symptoms,  
 XX and/or for inhibiting angiogenesis. This sequence corresponds to a  
 XX therapeutic untranslated region used in the invention.

Sequence 1192 BP; 378 A; 177 C; 169 G; 468 T; 0 U; 0 Other;  
 Query Match 92.0%; Score 18.4; DB 13; Length 1192;  
 Best Local Similarity 95.0%; Pred. No. 27;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCAA 20  
 | | | | | | | | | | | | | | | | | | | | | |  
 DB 49 AATGAGCCACCACTGTCCAA 30

RESULT 8  
 ADB59258/c  
 ID ADB59258 standard; DNA; 2711 BP.  
 XX  
 XX ADB59258;  
 XX  
 XX 04-DEC-2003 (first entry)  
 XX  
 XX Toxicity-related gene, SEQ ID 4284.  
 XX  
 XX Toxic; toxin; gene expression profile; hepatotoxicity; liver;  
 XX drug screening; toxicity assay; de.  
 XX  
 XX Unidentified.  
 XX  
 XX WO2003064624-A2.  
 XX  
 XX 07-AUG-2003.  
 XX  
 XX 31-JAN-2003; 2003WO-US003194.  
 XX  
 XX 31-JAN-2002; 2002US-00060087.  
 XX 15-MAR-2002; 2002US-0364045P.  
 XX 15-MAR-2002; 2002US-0364055P.  
 XX 30-DEC-2002; 2002US-0436643P.  
 XX  
 XX (GENE-) GENE LOGIC INC.  
 XX  
 XX Mandrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;  
 XX WPI; 2003-689530/65.  
 XX  
 XX Predicting a toxic effect of a compound, useful in identifying toxicity  
 XX markers in liver tissues or cells for drug screening and toxicity assays,  
 XX comprises preparing gene expression profile of tissue or cells exposed to  
 XX the compound.  
 XX  
 XX Claim 1; SEQ ID NO 4284; 1156pp; English.  
 XX  
 XX The present invention relates to a method for predicting a toxic effect  
 XX of a compound. The method comprises preparing a gene expression profile  
 XX of a tissue or cell sample exposed to the compound, and comparing the  
 XX gene expression profile to a database comprising SEQ ID 1-4925, where

CC differential expression of the gene indicates at least one toxic effect.  
CC The method is useful for predicting at least one toxic effect of a  
CC compound, predicting hepatotoxicity or the progression of a toxic effect  
CC of a compound, identifying an agent that modulates the onset or  
CC progression of a toxic response, predicting the cellular pathways that a  
CC compound modulates in a cell, and identifying an agent that modulates at  
CC least one activity of a protein. The method and compositions of the  
CC present invention using a database of genes having liver toxin-induced  
CC differential expression, are useful in identifying toxicity markers in  
CC liver tissues or cells for drug screening and toxicity assays. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 2711 BP; 798 A; 613 C; 623 G; 677 T; 0 U; 0 Other;

QY Query Match 92.0%; Score 18.4; DB 10; Length 2711;  
Best Local Similarity 95.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 AATGAGCCACCACTGTCCAA 20  
2707 AGTGAGCCACCACTGTCCAA 2688

## RESULT 9

AB054551/C  
ID AB054551 standard; cDNA; 2861 BP.

XX AB054551;

XX 22-AUG-2002 (first entry)

DE Human ovarian antigen HMORJ10 cDNA, SEQ ID NO:431.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
XX ovarian cancer; breast cancer; tumour; reproductive system disorder;  
XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
XX PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
XX inflammatory condition; immune disorder; blood disorder;  
XX cardiovascular disorder; respiratory disorder; neurological disorder;  
XX gastrointestinal disorder; urinary system disorder; drug screening;  
XX gene therapy; chromosome mapping; forensic analysis;  
XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
XX antiinflammatory; gynaecological; reproductive; chromosome 14q21-24;  
XX gene; ss.

XX Homo sapiens.

XX MO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US018569.

XX 07-JUN-2000; 2000US-0209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Bliese CR, Rosen CA;

XX WPI; 2002-147878/19.

XX F-PSDB; ABP41474.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
XX useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian  
XX cancer), immune disorders, cardiovascular disorders and neurological  
XX diseases.

XX Claim 1; SEQ ID NO 431; 2922BP; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
XX ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also

CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
CC to the sequences of the invention. The invention additionally relates to  
CC recombinant vectors and host cells comprising human ovarian antigen  
CC polynucleotides, antibodies against human ovarian antigens, and the use  
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
CC treating, prognosing or preventing various ovary and/or breast-related  
CC disorders. Such conditions include ovarian cancer and breast cancer, and  
CC metastatic tumours of ovarian or breast origin, reproductive system  
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
CC vaginitis), immune disorders (e.g., congenital and acquired  
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
CC respiratory disorders, neurological disorders, gastrointestinal disorders  
CC and urinary system disorders. Ovarian antigen polypeptides and  
CC polynucleotides may also be used in screening for compounds which  
CC modulate ovarian antigen expression or activity. The polynucleotides may  
CC further be used for gene therapy, chromosome mapping, in the  
CC identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as food additives or to prepare antibodies  
CC useful in disease diagnosis, drug targeting and phenotyping. The present  
CC sequence represents cDNA encoding a human ovarian antigen of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 2861 BP; 960 A; 539 C; 484 G; 877 T; 0 U; 1 Other;

QY Query Match 92.0%; Score 18.4; DB 6; Length 2861;  
Best Local Similarity 95.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 AATGAGCCACCACTGTCCAA 20  
1677 AGTGAGCCACCACTGTCCAA 1658

## RESULT 10

AD116279/C  
ID AD116279 standard; DNA; 3203 BP.

XX AD116279;

XX 22-APR-2004 (first entry)

DE Human nucleic acid-associated protein (NAP) coding sequence #14.

XX human; nucleic acid-associated protein; NAP; autoimmune disorder;  
XX inflammatory disorder; AIDS; allergy; infection; metabolic disorder;  
XX obesity; reproductive disorder; infertility; neurological disorder;  
XX Parkinson's disease; Alzheimer's disease; cardiovascular disorder;  
XX myocardial infarction; hypertension; eye disorder;  
XX cell proliferative disease; cancer; ds; gene.

XX Homo sapiens.

XX MO2003094848-A2.

XX 20-NOV-2003.

XX 09-MAY-2003; 2003WO-US014450.

XX 10-MAY-2002; 2002US-0379843P.

XX 24-MAY-2002; 2002US-0383457P.

XX 31-MAY-2002; 2002US-0384699P.

XX 06-JUN-2002; 2002US-0387265P.

XX (INCY-) INCYTE CORP.

XX Kable AE, Elliott VS, Tran UK, Ramkumar J, Margulis JP, Chawla NK,  
XX Richardson TW, Bulloch SA, Khare R, Lee SY, Lal PG, Tang YT, Yue H;



P1	Sivernakar A., Becha SD, Hatella AJA, Chang H, Baughn MR, Borowsky NT,
P1	Gietzen KU, He A, Forsyth J, Sprague WW, Blake JJ, Warren BA,
P1	Mason PM, Ison CH, Lindquist EA, Wilson AD, Jin P;
XX	WPI; 2004-011999/01.
DR	P-PSDBJ; ADI16229.
XX	
PT	New human nucleic acid associated proteins and polynucleotides, useful
PT	for diagnosing, preventing or treating diseases or conditions associated
PT	with aberrant protein expression, e.g. cancer, AIDS, atherosclerosis or
PT	stroke.
XX	
PS	Claim 5; SEQ ID NO 64; 400bp; English.
XX	
CC	The invention comprises the amino acid and coding sequences of human
CC	nucleic acid-associated proteins (NAAP). The DNA and protein sequences of
CC	the invention are useful in diagnosing, preventing and treating
CC	diseases/conditions associated with altered expression of NAAP, such as:
CC	autoimmune/inflammatory disorders (e.g. AIDS and allergies), infections
CC	(e.g. bacterial and viral), metabolic disorders (e.g. obesity),
CC	reproductive disorders (e.g. infertility), neurological disorders (e.g.
CC	Parkinson's disease and Alzheimer's disease), cardiovascular disorders
CC	(e.g. myocardial infarction and hypertension), eye disorders, or cell
CC	proliferative diseases (e.g. cancer). The present DNA sequence encodes a
CC	human NAAP protein of the invention.
XX	
SEQ	Sequence 3203 BP, 978 A; 691 C; 653 G; 861 T; 0 U; 0 Other;

Query Match	92.0%	Score 18.4	DB 12	Length 3203
Best Local Similarity	95.0%	Pred. No. 31		
Matches 19, Conservative	0	Mismatches 1	Indels 0	Gaps 0

```

QY      1  AATGAGCCACCAGTGTCCAA  20
        | | | | | | | | | | | |
Db      2766 AGTGAGCCACCAGTGTCCAA  2747

```

RESULT 11  
ADA24506/c  
ID ADA24506 standard; cDNA; 3229 BP.

DT 20-NOV-2003 (first entry)

Human cDNA differential expressed in adipose tissue, INCYTE1250434CBI.

OS Homo sapiens.

PN US2003096272-A1

PD 22-MAY-2003

PF 29-JUL-2002; 2002US-00208408.

PR 30-JUL-2001; 2001US-0308868P.

PA (INCY-) INCYTB GENOMICS INC.

PI Schebye XM,

DR WPI; 2003-606416/57.

PT New combination comprising several cDNAs, useful for preparing a PT composition for diagnosing or treating diabetes mellitus, obesity, PT hypertension, atherosclerosis, or cancer of the breast, prostate or PT colon.

XX	
PS	Claim 1; Page 46-47; 84pp; English
VV	

CC Then invention relates to a new combination comprising 55 CDNA (ADD2444655  
CC ADNA539) or their complements that are differentially regulated in an  
CC adipose sample. Also included are detecting differential expression of  
CC one or more CDNA in a sample containing nucleic acid, screening several  
CC molecules or compounds to identify a ligand that specifically binds a  
CC cDNA, a vector comprising the cDNA, a host cell containing the vector,  
CC producing a protein, screening several molecules or compounds, producing  
CC an antibody and the isolated antibody. The cDNAs comprise sequences which  
CC are upregulated or downregulated in response to peroxisome proliferator-  
CC activated receptor gamma (PPARgamma) agonist. The combination comprising  
CC several cDNAs is useful for preparing a composition for diagnosing or  
CC treating diabetes mellitus, obesity, hypertension, atherosclerosis,  
CC cancer of the breast, prostate or colon, or polycystic ovarian syndrome.  
XX

Query Match	92.0%	Score 18.4	DB 9	Length 3229
Best Local Similarity	95.0%	Pred. No. 31		
Matches 19, Conservative	0	Mismatches 1	Indels 0	Gaps 0

```

QY      1 AATGAGCCACCACTGTCCA 20
          |||||
Db      2794 AGTGAGCCACCACTGTCCA 2775

```

RESULT 12  
ADE25615/c  
ID ADE25615 standard; cDNA; 3229 BP.

DT 29-JAN-2004 (first entry)

DE Human cDNA differentially expressed in foam cells #19.

KW Human; ss; differential expression; foam cell; LPS; lipopolysaccharide;  
KW cardiovascular disease; atherosclerosis.

OS Homo sapiens.

PN US2003194721-A1.

PD 16-OCT-2003

PF 18-SEP-2002; 2002US-00247671

PR 19-SEP-2001; 2001US-0323784P

PA (INCY-) INCYTE GENOMICS INC.

PI Mikita T, Shiffman D, Porter JG, Kaser MR;

DR WPI; 2003-875398/81.

22

PT Combination containing several polynucleotide that are differentially expressed in foam cells and complements of the polynucleotides, useful for diagnosing cardiovascular disease or atherosclerosis.

PS Claim 1; SEQ ID NO 19; 37pp; English.

The invention relates to a combination comprising several polynucleotides having any one of 127 sequences (S1) such as the sequence of human calmodulin gene, human mRNA for KIRAO930 protein, leukocyte A4 hydrolase, human GGI-142 protein mRNA, human K<sup>+</sup> channel beat 2 subunit mRNA, etc., and their complements. The cDNAs are differentially expressed in LPS (lipopolysaccharide)-treated foam cells. Also included are obtaining an extended or full length gene from a library of nucleic acid sequences, an expression vector containing the nucleic acids, a host cell containing the vector, a purified polypeptide appearing as ADR25750 and

CC ADE25751, producing a protein by culturing the host cell, and a  
CC composition comprising a purified antibody that specifically binds to the  
CC protein. The foam cell-expressed nucleic acids are useful for a high  
CC throughput detection of differential expression of one or more  
CC polynucleotides in a sample. The sample is from a subject with  
CC atherosclerosis and comparison with a standard defines early, mid or late  
CC stages of the disorder. The foam cell-expressed nucleic acids are useful  
CC for high throughput screening of a library of molecules or compounds to  
CC identify a ligand which binds a polynucleotide. The library is chosen  
CC from DNA molecules, peptides, proteins and RNA molecules. The protein is  
CC useful for a high throughput screening of library of molecules or  
CC compounds to identify at least one ligand which specifically binds a  
CC protein, for purifying a ligand from a sample for making an antibody. The  
CC foam cell-expressed nucleic acids are useful for diagnosing  
CC cardiovascular disorder. The foam cell-expressed nucleic acids are useful  
CC as elements on a microarray which can be used for detecting related  
CC polynucleotides in a sample, diagnosing cardiovascular disease,  
CC atherosclerosis. The present sequence represents a cDNA whose expression  
CC is upregulated in LPS treated foam cells.

CC Sequence 3229 BP; 987 A; 695 C; 658 G; 889 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 10; Length 3229;  
Best Local Similarity 95.0%; Pred. No. 31;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCACTGTCCAA 20  
Db 2794 AGTGAGCCACCACTGTCCAA 2775

RESULT 13

ADJ56307/c  
ID ADJ56307 standard; cDNA; 3229 BP.

AC ADJ56307;

XX 06-MAY-2004 (first entry)

DE Human cDNA differentially expressed in MYCN activated cells Segid 113.

XX human; differential expression; transactivator; proto-oncogene;

KM neuroblastoma; small cell lung cancer; cytostatic; gene therapy; ss;

XX MYCN activated cell.

OS Homo sapiens.

XX US2003119009-A1.

XX 26-JUN-2003.

XX 25-FEB-2002; 2002US-00084817.

XX 23-FEB-2001; 2001US-0270784P.

XX (STUD/) STUART S G.

XX (NUCH/) NUCHTERN J G.

XX (PLON/) PLON S E.

XX (SHOH/) SHOHEI J M.

XX Stuart SG, Nuchtern JG, Plon SB, Shohet JM;

XX WPI, 2003-635698/60.

XX New genes regulated by MYCN activation, useful in gene therapy,

XX particularly for treating a subject with e.g. neuroblastoma or other

XX cancer, or for diagnosing, staging or monitoring the treatment of the

XX cancer.

XX Claim 1; SEQ ID NO 113; 27pp; English.

XX This invention relates to novel isolated cDNAs that are differentially

XX expressed in MYCN activated cells. Specifically, it refers to

CC polynucleotide sequences that exhibit differential expression patterns in  
CC cells activated by the transactivator MYCN, where MYCN is a proto-  
CC oncogene that is amplified in neuroblastoma cells and is common in small  
CC cell lung cancers. The present invention describes these cDNA molecules  
CC as useful for in hybridisation assays to detect expression of nucleic  
CC acids (or complementary nucleic acids) in a present in a given sample, as  
CC well as for screening assays by identifying molecules or compounds that  
CC specifically bind the cDNA as a ligand and modulate function or activity.  
CC Accordingly, these compositions exhibit cytostatic activity and can also  
CC be used for gene therapy purposes. This polynucleotide sequence is a cDNA  
CC that is differentially expressed in MYCN activated cells, given in an  
CC exemplification of the invention. NOTE: This sequence does not appear in  
CC the printed specification but has been obtained in electronic format from  
CC the US Patent Office at  
CC ftp.seqdata.uspto.gov/sequence.html?DocID=20030119009.

CC Sequence 3229 BP; 987 A; 695 C; 658 G; 889 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 10; Length 3229;  
Best Local Similarity 95.0%; Pred. No. 31;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCACTGTCCAA 20  
Db 2794 AGTGAGCCACCACTGTCCAA 2775

RESULT 14

ADJ76983/c  
ID ADJ76983 standard; cDNA; 3229 BP.

AC ADJ76983;

XX 29-JAN-2004 (first entry)

DE Human cDNA differentially expressed in a liver disorder #106.

XX human; ss; gene; liver disorder; hyperlipidaemia; hypertension;

KM type II diabetes; tumour; liver; inflammatory disorder;

KM immune response disorder; high-throughput screening;

XX differential gene expression; gene therapy.

OS Homo sapiens.

XX US2003108871-A1.

XX 12-JUN-2003.

XX 30-JUL-2001; 2001US-00919039.

XX 28-JUL-2000; 2000US-0222113P.

XX (KASE/) KASER M R.

XX Kaser MR;

XX WPI; 2004-031227/03.

XX P-PSDB; ADE76984.

XX Composition comprising several cDNAs that are differentially expressed in

XX treated human C3A liver cell cultures, useful for treating liver

XX disorders.

XX Claim 1; SEQ ID NO 148; 41pp; English.

XX The invention relates to a composition comprising several cDNAs that are

XX differentially expressed in a liver disorder. The composition is useful

XX for treating liver disorder such as hyperlipidaemia, hypertension, type

XX II diabetes, tumours of the liver and disorders of the inflammatory and

XX immune response. The composition is useful for a high-throughput method

XX of screening several molecules or compounds to identify a ligand which

XX specifically binds a cDNA. A protein encoded by the cDNA is useful for a

XX high-throughput method for using a protein to screen several molecules or



GenCore version 5.1.8  
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OM nucleic - nucleic search, using BW model

Run on: May 21, 2006, 21:16:50 ; Search time 2223.5 Seconds  
(without alignments)  
502.985 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagcaccacgtccca 20

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_est7:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gss1:\*  
12: gb\_gss2:\*  
13: gb\_gss3:\*  
14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	238 7	BE764191 IL5-NT007
2	20	100.0	250 7	BE764172 IL5-NT007
3	20	100.0	255 8	CV826845 EST001143
4	20	100.0	266 7	BE764166 IL5-NT007
5	20	100.0	317 7	BE712842 WR0-HT09
6	20	100.0	344 7	BE160136 QV1-HT041
7	20	100.0	347 9	DN130625
8	20	100.0	375 10	DY153390
9	20	100.0	378 5	CD288829
10	20	100.0	389 10	DY112562
11	20	100.0	394 4	BE925260
12	20	100.0	492 10	DV769093
13	20	100.0	537 1	AJ683529
14	20	100.0	545 2	BE923330
15	20	100.0	560 9	CX593021
16	20	100.0	591 9	DN402969
17	20	100.0	596 9	DA541613
18	20	100.0	613 10	DY085271
19	20	100.0	613 10	DY085271

c 20	20	100.0	634 8	CK978607	CK978607 4110096 B
c 21	20	100.0	653 8	CK947392	CK947392 4071959 B
c 22	20	100.0	657 8	CN264295	CN264295 170006000
c 23	20	100.0	661 1	AJ746976	AJ746976 AJ746976
c 24	20	100.0	681 4	CB118713	CB118713 K-EST0185
c 25	20	100.0	683 7	BF042862	BF042862 BP250019B
c 26	20	100.0	696 5	CK962009	CK962009 4076289 B
c 27	20	100.0	696 10	DT895390	DT895390 1478415 M
c 28	20	100.0	701 9	DN395152	DN395152 LIB3935-0
c 29	20	100.0	725 1	AJ955413	AJ955413 AJ955413
c 30	20	100.0	726 8	CN264320	CN264320 170004277
c 31	20	100.0	737 4	CD103310	CD103310 AGENCOURT
c 32	20	100.0	750 1	AV702635	AV702635 AV702635
c 33	20	100.0	751 2	BG112073	BG112073 602283241
c 34	20	100.0	753 10	DV830978	DV830978 LB01917.C
c 35	20	100.0	772 4	CB312460	CB312460 AGENCOURT
c 36	20	100.0	786 9	DN425733	DN425733 LIB4216-0
c 37	20	100.0	788 4	CD110467	CD110467 AGENCOURT
c 38	20	100.0	788 5	CJ462062	CJ462062 CJ462062
c 39	20	100.0	804 10	DV873369	DV873369 LB02520.C
c 40	20	100.0	818 2	BG108056	BG108056 602279983
c 41	20	100.0	824 1	AJ950688	AJ950688 AJ950688
c 42	20	100.0	835 10	DV834747	DV834747 LB0196.CR
c 43	20	100.0	861 1	AJ945476	AJ945476 AJ945476
c 44	20	100.0	908 10	DV921086	DV921086 LB02923.C
c 45	20	100.0	923 2	BG108209	BG108209 602280087

#### ALIGNMENTS

RESULT 1  
BE764191/c 238 bp mRNA linear EST 19-SEP-2000  
LOCUS IL5-NT0071-200600-106-h11 NT0071 Homo sapiens CDNA, mRNA sequence.  
DEFINITION BE764191  
ACCESSION BE764191.1 GI:10194115  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
1 (bases 1 to 238)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W.J.F., Zago, M.A., Bordin, S., Costa, F.E., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the P4PSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-IL5-NT0071-200600-106-h11&t3=2000-06-20&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 59  
High quality sequence stop: 238.  
Location/Qualifiers  
1. 238  
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/mol\_type="mRNA"

/db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="NT0071"  
 /note="Organ: nervous tumor; Vector: puc18; Site: 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 64;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTAA 20  
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 Db 156 AATGAGCCACCAAGTGTCCTAA 137

## RESULT 2

LOCUS BE764172 250 bp mRNA linear EST 19-SEP-2000  
 DEFINITION IL5-NT0071-200600-106-c10 NT0071 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BE764172  
 VERSION BE764172.1 GI:10194096  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

## REFERENCE

1 (bases 1 to 250)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags

## TITLE

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## JOURNAL

## PUBLISHED

## COMMENT

Contact: Simpson A.J.J.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=et2=IL5-NT0071-200  
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Seq primer: puc 18 forward

High quality sequence stop: 250.

## FEATURES

## source

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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="NT0071"

/note="Organ: nervous tumor; Vector: puc18; Site: 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTAA 20  
 |||||  
 Db 83 AATGAGCCACCAAGTGTCCTAA 102

## RESULT 3

## LOCUS

CV826845/c 255 bp mRNA linear EST 13-DEC-2004  
 DEFINITION EST001143 brain and spinal cord cDNA library in Gecko Gekko  
 japonicus cDNA clone SJ15D12, mRNA sequence.

ACCESSION CV826845  
 VERSION CV826845.1 GI:55776384  
 KEYWORDS EST.  
 SOURCE Gekko japonicus

## ORGANISM

Gekko japonicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Lepidodonta; Squamata; Scleroglossa; Gekkota; Gekkonidae; Gekko.  
 1 (bases 1 to 255)  
 Gu, X., Ding, F., Liu, Y., Liu, M., Shen, M., Gong, L., Zhang, Q., Tang, X.  
 and Yang, H.

Analysis of expressed sequences tags and cloning of full length  
 cDNA from brain and spinal cord cDNA library in Gecko (2004)

## JOURNAL

## COMMENT

Contact: Gu Xiaosong

The Key Laboratory of Neuroregeneration of Jiangsu Province

Nantong Medical College

Qixiu Road 19, Nantong city, Jiangsu Province, P.R.China

Tel: 86-513-5051800

Fax: 86-513-5511585

Email: neuron@public.nt.js.cn.

## FEATURES

## source

1..255  
 Location/Qualifiers  
 /organism="Gekko japonicus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:146911"  
 /clone="SJ15D12"  
 /tissue\_type="brain and spinal cord"  
 /clone\_lib="brain and spinal cord cDNA library in Gecko"

## ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTAA 20  
 |||||  
 Db 234 AATGAGCCACCAAGTGTCCTAA 215

## RESULT 4

## LOCUS

BE764166/c 266 bp mRNA linear EST 19-SEP-2000  
 DEFINITION IL5-NT0071-200600-106-b05 NT0071 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BE764166  
 VERSION BE764166.1 GI:10194090  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 266)

## REFERENCE

## AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.J.

**TITLE** Shotgun sequencing of the human transcriptome with ORF expressed  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
**PUBLISHED** 10737800  
**COMMENT** Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=IL5-NT0071-200  
 600-106-b05et3=2000-06-20et4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 266.  
**FEATURES**  
 source  
 1. 266  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="NT0071"  
 /notes="Organ: nervous tumor; Vector: puc18; Site: 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
**ORIGIN**  
 Query Match 100.0%; Score 20; DB 7; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AATGAGCCACCAGTGTCCTAA 20  
 |||||  
 Db 168 AATGAGCCACCAGTGTCCTAA 149  
**RESULT 5**  
**LOCUS** BE712842 317 bp mRNA linear EST 12-SEP-2000  
**DEFINITION** M00-HT0699-060800-001-h09 HT0699 Homo sapiens cDNA, mRNA sequence.  
**ACCESSION** BE712842  
**VERSION** BE712842.1 GI:10101107  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 317)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
**REFERENCE**  
**AUTHORS** Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 10737800  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=MR0-HT0699-060  
 800-001-h09et3=2000-08-06et4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 14  
 High quality sequence stop: 317.  
**FEATURES**  
 source  
 1. 317  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="HT0699"  
 /notes="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
**ORIGIN**  
 Query Match 100.0%; Score 20; DB 7; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AATGAGCCACCAGTGTCCTAA 20  
 |||||  
 Db 149 AATGAGCCACCAGTGTCCTAA 168  
**RESULT 6**  
**LOCUS** BE160136 327 bp mRNA linear EST 21-JUN-2000  
**DEFINITION** QV1-HT0412-290400-178-h08 HT0412 Homo sapiens cDNA, mRNA sequence.  
**ACCESSION** BE160136  
**VERSION** BE160136.1 GI:8622857  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 327)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
**REFERENCE**  
**AUTHORS** Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 10737800  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=QV1-HT0412-290  
 400-178-h08et3=2000-04-29et4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 78.  
**FEATURES**  
 source  
 1. 327  
 Location/Qualifiers  
 /organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0412"
/notes="Organ: head neck; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

## ORIGIN

```

Query Match      100.0%; Score 20; DB 7; Length 327;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTAA 20
    |||||
Db 63 AATGAGCCACCAAGTGTCCTAA 82

```

## RESULT 7

```

LOCUS      DN130625      344 bp      mRNA      linear      EST 15-FEB-2005
DEFINITION 1147199 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
ACCESSION  DN130625
VERSION     DN130625.1 GI:59824906
KEYWORDS   EST.
SOURCE     Sus scrofa (pig)
ORGANISM   Sus scrofa

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

```

## REFERENCE

```

1 (bases 1 to 344)
Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Nonneman,D.J., Wray,J.E. and Keele,J.W.
Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
Unpublished (2003)

```

## JOURNAL

## COMMENT

```

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_ait option. Vector identified with
cross_match v0.990329.
Plate: HHY8037 row: A column: 11
Seq primer: TAGAGGCACAGTCGAGG.

```

## FEATURES

```

source
1..344
Location/Qualifiers
1..344
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH108"
/clone_lib="MARC 4PIG"
/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

```

## ORIGIN

```

Query Match      100.0%; Score 20; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTAA 20
    |||||
Db 98 AATGAGCCACCAAGTGTCCTAA 117

```

## RESULT 8

```

LOCUS      DY153390/c      375 bp      mRNA      linear      EST 01-FEB-2006
DEFINITION 000705EMPA002625HT BMPA Bos taurus cDNA, mRNA sequence.
ACCESSION  DY153390
VERSION     DY153390.1 GI:86347565
KEYWORDS   EST.
SOURCE     Bos taurus (cattle)
ORGANISM   Bos taurus

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 375)
McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.,
Hagemann,L., Lee,R., Hein,W., Johnstone,P., Macpool,N., McMahon,C.,
McCracken,J., Steiwagen,K., Farr,V., Singh,K., Whitley,J.,
Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
Wells,M., Bowman,P., Goddard,M., Langford,C., McSwan,J. and
Atkinson,P.

```

## REFERENCE

## AUTHORS

## JOURNAL

## COMMENT

## FEATURES

## source

## Location/Qualifiers

## 1..375

## /organism="Bos taurus"

## /mol\_type="mRNA"

## /db\_xref="taxon:9913"

## /tissue\_type="Pre-Partum mammary"

## /clone\_lib="BMPA"

## /note="Vector: pBK-CMV; Bovine 85 days pre-partum mammary

## tissue cDNA library derived from tissue harvested from an

## Angus cow by Adrian Molenaar on 01/01/00"

## Angus cow by Adrian Molenaar on 01/01/00"

## Angus cow by Adrian Molenaar on 01/01/00"

## Angus cow by Adrian Molenaar on 01/01/00"

## Angus cow by Adrian Molenaar on 01/01/00"

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## Angus cow by Adrian Molenaar on 01/01/00"

## Angus cow by Adrian Molenaar on 01/01/00"

## Angus cow by Adrian Molenaar on 01/01/00"

USA  
Tel: 9798454896  
Fax: 9798622862  
Email: tpencerc@ansc.tamu.edu.

## FEATURES

## Source

1. .378  
/organism="Ovis aries"  
/mol\_type="mRNA"  
/db\_xref="taxon:9940"  
/sex="Female"  
/tissue\_type="endometrium"  
/dev\_stage="Day 14 pregnant"  
/clone\_lib="POE14 (Day 14 pregnant ovine endometrium)"  
/note="Organ: uterus; Vector: Triplex2; Site\_1: EcorI;  
Site\_2: XhoI; Non-normalized library, sequenced 5' with  
Triplex2 primer (CTCCGAGTCTGGACGAGC). Library constructed  
by Clontech with total RNA extracted using the Trizol  
method and pooled from 5 females."

## ORIGIN

Query Match 100.0%; Score 20; DB 5; Length 378;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAGTGTCCTCA 20  
Db 351 AATGAGCCACCAGTGTCCTCA 332

## RESULT 10

## DY112562/c

LOCUS DY112562/c 389 bp mRNA linear EST 01-FEB-2006  
DEFINITION 000222BOVB005432HT BOVB Bos taurus CDNA, mRNA sequence.  
ACCESSION DY112562  
VERSION DY112562.1 GI:86275839  
KEYWORDS EST.  
SOURCE Bos taurus (cattle)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.

## REFERENCE

## AUTHORS

McClulloch, A., Wilson, T., Molenaar, A., Grigor, M., Davis, S.,  
Glenn, M., Havukkala, I., Watson, J., Crawford, A., Wheeler, T.,  
Hagemann, L., Lee, R., Hein, W., Johnstone, P., Macgibbon, N., McMahon, C.,  
McCracken, J., Stelwagen, K., Farr, V., Singh, K., Whitley, J.,  
Nicholas, K., Savin, K., Mather, A., McPartlan, H., Whitley, J.,  
Wells, M., Bowman, P., Goddard, M., Langford, C., McEwan, J. and  
Atkinson, P.

AgResearch, Genesis and Primary Industry Victoria Bovine EST  
project

## JOURNAL

Unpublished (2006)

## COMMENT

Contact: Macgibbon N  
AgResearch Ltd.  
Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,  
Mosgiel, New Zealand  
Email: nauman.macgibbon@agresearch.co.nz.

## FEATURES

## Source

1. .389  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="Ovarian"  
/clone\_lib="BOVB"  
/notes="Vector: pBK-CMV; Bovine ovary cDNA library derived  
from tissue harvested from an unknown breed calf by Allan  
Crawford on 28/09/99"

## ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 389;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAGTGTCCTCA 20  
Db 152 AATGAGCCACCAGTGTCCTCA 133

## RESULT 11

## BE925260

LOCUS BE925260 394 bp mRNA linear EST 02-OCT-2000  
DEFINITION CM4-AN0081-210800-274-d01 AN0081 Homo sapiens CDNA, mRNA sequence.  
ACCESSION BE925260  
VERSION BE925260.1 GI:10451336  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

## REFERENCE

## AUTHORS

1 (bases 1 to 394)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,  
Goldman, G.H., Carvalho, A.P., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, P., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the PAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=CM4-AN0081-210  
800-274-d01&tl3=2000-08-21&tl4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 24  
High quality sequence stop: 392.

## TITLE

## JOURNAL

## PUBMED

## COMMENT

## FEATURES

## Source

1. .394  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/dev\_stage="Adult"  
/clone\_lib="AN0081"  
/notes="Organ: amnion normal; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 394;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAGTGTCCTCA 20  
Db 89 AATGAGCCACCAGTGTCCTCA 108

## RESULT 12

## CA778645/c

LOCUS CA778645 403 bp mRNA linear EST 03-DEC-2002  
DEFINITION MPL384\_10\_D22 MPL Sus scrofa cDNA clone pSPORT1 5', mRNA sequence.  
ACCESSION CA778645



```

VERSION
KEYWORDS
SOURCE
ORGANISM

CA778645.1 GI:26016521
EST.
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

1 (bases 1 to 403)
Center for Animal Functional Genomics.
Generation of ESTs from mixed pig cDNA libraries
Unpublished (2002)
JOURNAL
COMMENT
Contact: Steven P. Suchyta
Center for Animal Functional Genomics, Department of Animal Science
Michigan State University
B215 Anthony Hall, East Lansing, MI 48824, USA
Tel: 517 355 8443
Fax: 517 432 9168
Email: suchytas@msu.edu
Single pass sequencing. Bases called and alt-trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore
20 -minmatch 12 options.
Seq primer: T7.

FEATURES
source
Location/Qualifiers
1..403
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="pSPORT1"
/sex="Male and female"
/tissue_type="pooled"
/dev_stage="pooled"
/lab_host="DH10B"
/clone_lib="MPL"
/notes="Organ: pooled; Vector: pSPORT1; Site 1: NotI;
Site 2: SalI; Library made from pooled tissue from
adipose, adrenal gland, blood leukocytes, brain,
cartilage, eye, heart, intestine, kidney, liver, lung
lymph nodes, mammary gland, myogenic satellite cells,
ovary, pancreas, pituitary gland, placenta, skin, spinal
cord, spleen, stomach, tendon, testes, uterus, and
vascular from various developmental and physiological
stages."

ORIGIN
Query Match 100.0%; Score 20; DB 4; Length 403;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACAGTGTCCTCA 20
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Db 216 AATGAGCCACAGTGTCCTCA 197

RESULT 13
DV769093/c
LOCUS
DEFINITION
ILLUMIGEN MCQ 67822 Katze MMTV Macaca mulatta cDNA clone
|BIUW:39154 57 similar to Bases 5 to 392 highly similar to human
HIF1A (Hs.509554), mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.

1 (bases 1 to 492)
Magnes, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agv, M.B.,
Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
Iadonato, S.P.
JOURNAL
COMMENT
Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human

JOURNAL
PUBMED
COMMENT
Genome Biol. 6 (7), R60 (2005)
15998449
Contact: C. Magnes
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagnes@illumigen.com
Sequenced on 2005.08.01. 669 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org
PCR Primers
FORWARD: CCTCTACTAAGGGAACAAAA
BACKWARD: CACTATAGGCGCAATGGGTA
Insert Length: 492 Std Error: 0.00
Plate: CL000566 row: H column: 12
Seq primer: CCTCTACTAAGGGAACAAAA
POLYA=No.

FEATURES
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Location/Qualifiers
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/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUV:39154"
/sex="male"
/tissue_type="testis"
/dev_stage="juvenile"
/lab_host="Electronmax DH10B"
/clone_lib="Katze MMTV"
/notes="Vector: pDONR 222; Site 1: BspG I; Site 2: BspG I;
Created from CloneMiner cDNA Library Construction kit
(catalog #18249-029)"

ORIGIN
Query Match 100.0%; Score 20; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACAGTGTCCTCA 20
|||||
Db 417 AATGAGCCACAGTGTCCTCA 398

RESULT 14
AJ683529/c
LOCUS
DEFINITION
AJ683529 CSEQRAN04 Sus scrofa cDNA clone C0001802_F15, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

1 (bases 1 to 537)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
JOURNAL
COMMENT
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options. Vector: pBlueScriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13P Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Midlothian, UK,

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FEATURES  
source  
EH25 9PS, www.arkgenomics.org.  
Location/Qualifiers  
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/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001802\_F15"  
/tissue\_type="uterus"  
/clone\_lib="CSEQRAN04"  
/note="Vector: pBluescriptII (KS+); Site 1: EcoRI; Site 2:  
NotI; Single pass sequencing. Normalised library  
constructed from pig uterus."

## ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 537;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAGTGTCCAA 20  
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Db 214 AATGAGCCACCAGTGTCCAA 195

## RESULT 15

BF923330  
LOCUS  
DEFINITION MR2-NT0137-211100-005-a08 NT0137 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF923330  
VERSION BF923330.1 GI:12319218  
KEYWORDS EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

1 (bases 1 to 545)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

10737800

## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&tl2=MR2-NT0137-211100-005-a08&tl3=2000-11-21&tl4=1>)

Seq primer: puc 18 forward

High quality sequence stop: 543.

## FEATURES

source

1. .545  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="NT0137"

/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;  
Site 2: SnaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under

low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 545;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAGTGTCCAA 20  
|||||  
Db 424 AATGAGCCACCAGTGTCCAA 443

Search completed: May 21, 2006, 22:31:12  
Job time : 2227.5 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:18:10 ; Search time 79.5 Seconds  
(without alignments)  
470.719 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagccaccagtgtccaa 20

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_NA:\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5-COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A-COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B-COMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7-COMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H-COMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PPUS-COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP-COMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE-COMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.6	100.0	601	3	US-09-949-016-22571
C 2	19.6	100.0	601	3	US-09-949-016-52342
C 3	18.4	92.0	37	3	US-09-579-897-2
C 4	18.4	92.0	311	3	US-09-621-978-17247
C 5	18.4	92.0	601	3	US-09-949-016-22570
C 6	18.4	92.0	601	3	US-09-949-016-52341
C 7	18.4	92.0	2770	3	US-09-949-016-1518
C 8	18.4	92.0	3229	3	US-09-919-039-148
C 9	18.4	92.0	3678	3	US-09-380-662-22
C 10	18.4	92.0	3678	3	US-09-959-8738-19
C 11	18.4	92.0	3678	3	US-10-028-158-22
C 12	18.4	92.0	3736	2	US-08-480-4738-1
C 13	18.4	92.0	3736	3	US-08-915-213-1
C 14	18.4	92.0	3736	3	US-09-148-547-1
C 15	18.4	92.0	3736	3	US-09-235-217-1
C 16	18.4	92.0	3736	3	US-09-383-581-1
C 17	18.4	92.0	3736	7	PCR-US96-10251-1
C 18	18.4	92.0	3933	3	US-09-949-016-218
C 19	18.4	92.0	18120	3	US-09-949-016-13260
C 20	18.4	92.0	56714	3	US-09-949-016-11960
C 21	16.4	82.0	3924	3	US-09-023-655-1168
C 22	16.4	82.0	3924	3	US-09-762-195-2
C 23	16.4	82.0	3924	4	US-09-880-107-2299

24	16.4	82.0	97423	3	US-09-949-016-12742	Sequence 12742, A
25	16.4	82.0	97424	3	US-09-949-016-15576	Sequence 15576, A
C 26	16.4	82.0	390890	3	US-09-949-016-14720	Sequence 14720, A
27	16	80.0	2367	3	US-09-620-312D-1064	Sequence 1064, Ap
C 28	16	80.0	21721	3	US-09-269-939A-41	Sequence 41, Appl
C 29	16	80.0	22976	3	US-09-499-522-1	Sequence 19, Appl
C 30	16	80.0	23187	3	US-09-949-016-16080	Sequence 1, Appl
31	16	80.0	79858	3	US-09-949-016-115253	Sequence 16080, A
32	15.8	79.0	601	3	US-09-949-016-115254	Sequence 115253, A
33	15.8	79.0	601	3	US-09-949-016-115255	Sequence 115254, A
34	15.8	79.0	601	3	US-09-949-016-115255	Sequence 115255, A
C 35	15.8	79.0	601	3	US-09-949-016-115299	Sequence 115299, A
C 36	15.8	79.0	601	3	US-09-949-016-115300	Sequence 115300, A
37	15.8	79.0	17082	3	US-09-949-016-14893	Sequence 14893, A
C 38	15.8	79.0	37715	3	US-09-949-016-13846	Sequence 13846, A
C 39	15.8	79.0	47471	3	US-09-949-016-12271	Sequence 12271, A
C 40	15.8	79.0	113283	3	US-09-949-016-16976	Sequence 16976, A
C 41	15.8	79.0	113283	3	US-09-949-016-16977	Sequence 16977, A
C 42	15.8	79.0	119649	3	US-09-949-016-12537	Sequence 12537, A
C 43	15.8	79.0	135030	3	US-09-949-016-14896	Sequence 14896, A
C 44	15.4	77.0	601	3	US-09-949-016-176526	Sequence 176526, A
45	15.4	77.0	601	3	US-09-949-016-180123	Sequence 180123, A

#### ALIGNMENTS

##### RESULT 1

US-09-949-016-22571/c  
; Sequence 22571, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,769  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 22571  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-22571

Query Match 100.0%; Score 20; DB 3; Length 601;  
Best Local Similarity 95.0%; Pred. No. 1.2;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAGTGTCCAA 20

Db 302 ARTGAGCCACCAGTGTCCAA 283

##### RESULT 2

US-09-949-016-52342/c  
; Sequence 52342, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755

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/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 52342
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-949-016-52342

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 601;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 20
Db 302 ARTGAGCCACCAGTGTCCTCA 283

RESULT 3
US-09-579-897-2
/ Sequence 2, Application US/09579897
/ Patent No. 6432927
/ GENERAL INFORMATION:
/ APPLICANT: Gregory, Richard
/ APPLICANT: Vincent, Karen
/ TITLE OF INVENTION: Compositions and Methods for Inducing Gene Expression
/ FILE REFERENCE: GA0112CIP2
/ CURRENT APPLICATION NUMBER: US/09/579,897
/ CURRENT FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/067,546
/ PRIOR FILING DATE: 1997-12-04
/ PRIOR APPLICATION NUMBER: PCT/US98/25753
/ PRIOR FILING DATE: 1998-12-04
/ PRIOR APPLICATION NUMBER: 09/133,612
/ PRIOR FILING DATE: 1998-08-13
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2
/ LENGTH: 37
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-579-897-2

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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 20
Db 8 AGTGAGCCACCAGTGTCCTCA 27

RESULT 4
US-09-621-976-17247/c
/ Sequence 17247, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 17247
/ LENGTH: 311
/ TYPE: DNA

/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 52342
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-949-016-52342

Query Match
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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 20
Db 198 AGTGAGCCACCAGTGTCCTCA 179

RESULT 5
US-09-949-016-22570/c
/ Sequence 22570, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 22570
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-22570

Query Match
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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 20
Db 597 AGTGAGCCACCAGTGTCCTCA 578

RESULT 6
US-09-949-016-52341/c
/ Sequence 52341, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 52341
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-52341

Query Match
Best Local Similarity 92.0%; Score 18.4; DB 3; Length 601;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20
Db 597 AGTGAGCCACCAAGTGTCCAA 578

RESULT 7
US-09-949-016-1518/c
; Sequence 1518, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1518
; LENGTH: 2770
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1518

Query Match 92.0%; Score 18.4; DB 3; Length 2770;
Best Local Similarity 95.0%; Pred. No. 6.5;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20
Db 1647 AGTGAGCCACCAAGTGTCCAA 1628

RESULT 8
US-09-919-039-148/c
; Sequence 148, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 148
; LENGTH: 3229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 1250434CB1
US-09-919-039-148

Query Match 92.0%; Score 18.4; DB 3; Length 3229;
Best Local Similarity 95.0%; Pred. No. 6.6;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20
Db 2794 AGTGAGCCACCAAGTGTCCAA 2775

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 9
US-09-380-662-22/c
; Sequence 22, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 3678
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(2509)
US-09-380-662-22

Query Match 92.0%; Score 18.4; DB 3; Length 3678;
Best Local Similarity 95.0%; Pred. No. 6.8;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20
Db 2555 AGTGAGCCACCAAGTGTCCAA 2536

RESULT 10
US-09-959-873B-19/c
; Sequence 19, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 3678
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-959-873B-19

Query Match 92.0%; Score 18.4; DB 3; Length 3678;
Best Local Similarity 95.0%; Pred. No. 6.8;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCAA 20
Db 2555 AGTGAGCCACCAAGTGTCCAA 2536

RESULT 11
US-10-028-158-22/c
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Sequence 22, Application US/10028158  
Patent No. 6863880  
GENERAL INFORMATION:  
APPLICANT: Caniggia, Isabella  
APPLICANT: Post, Martin  
APPLICANT: Lye, Stephen  
TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF  
FILE OF INVENTION: TROPHOBLAST  
FILE REFERENCE: 11757.38USWO  
CURRENT APPLICATION NUMBER: US/10/028.158  
CURRENT FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: US/09/380,662  
PRIOR FILING DATE: 1999-12-21  
PRIOR APPLICATION NUMBER: PCT/CA98/00180  
PRIOR FILING DATE: 1998-03-05  
PRIOR APPLICATION NUMBER: US 60/039,919  
PRIOR FILING DATE: 1997-03-07  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 22  
LENGTH: 3678  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (29)..(2509)  
US-10-028-158-22

Query Match 92.0%; Score 18.4; DB 3; Length 3678;  
Best Local Similarity 95.0%; Pred. No. 6.8;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 20  
DB 2555 AGTGAGCCACCAGTGTCCTCA 2536

RESULT 12  
US-08-480-473B-1/c  
Sequence 1, Application US/08480473B  
Patent No. 5882914  
GENERAL INFORMATION:  
APPLICANT: Semenza, Gregg L.  
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,473B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/053001  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3736 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-480-473B-1

Query Match 92.0%; Score 18.4; DB 2; Length 3736;  
Best Local Similarity 95.0%; Pred. No. 6.8;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 20  
DB 2555 AGTGAGCCACCAGTGTCCTCA 2536

RESULT 13  
US-08-915-213-1/c  
Sequence 1, Application US/08915213  
Patent No. 6020462  
GENERAL INFORMATION:  
APPLICANT: Semenza, Gregg L.  
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/915,213  
FILING DATE: 20-AUG-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/480,473  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/053001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3736 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-915-213-1

Query Match 92.0%; Score 18.4; DB 3; Length 3736;  
Best Local Similarity 95.0%; Pred. No. 6.8;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 20  
DB 2555 AGTGAGCCACCAGTGTCCTCA 2536

RESULT 14  
US-09-148-547-1/c  
Sequence 1, Application US/09148547  
Patent No. 6124131  
GENERAL INFORMATION:  
APPLICANT: Semenza, Gregg L.  
TITLE OF INVENTION: Hypoxia Inducible Factor-1 and Methods of Use  
FILE REFERENCE: 07265/151001

Search completed: May 21, 2006, 21:21:00  
Job time : 81.5 secs

1 CURRENT APPLICATION NUMBER: US/09/148,547  
1 CURRENT FILING DATE: 1998-08-25  
1 NUMBER OF SEQ ID NOS: 2  
1 SOFTWARE: PatentIn Ver. 2.0  
1 SEQ ID NO 1  
1 LENGTH: 3736  
1 TYPE: DNA  
1 ORGANISM: Homo sapiens  
1 FEATURE:  
1 NAME/KEY: CDS  
1 LOCATION: (29)..(2509)  
US-09-148-547-1

Query Match 92.0%; Score 18.4; DB 3; Length 3736;  
Best Local Similarity 95.0%; Pred. No. 6.8;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGCCAA 20  
DB 2555 AGTGAGCCACCAGTGCCAA 2536

RESULT 15  
US-09-235-217-1/C  
1 Sequence 1, Application US/09235217  
1 Patent No. 6222018  
1 GENERAL INFORMATION:  
1 APPLICANT: Semenza, Gregg L.  
1 TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE  
1 NUMBER OF SEQUENCES: 64  
1 CORRESPONDENCE ADDRESS:  
1 ADDRESSEE: Fish & Richardson P.C.  
1 STREET: 4225 Executive Square, Suite 1400  
1 CITY: La Jolla  
1 STATE: CA  
1 COUNTRY: USA  
1 ZIP: 92037  
1 COMPUTER READABLE FORM:  
1 MEDIUM TYPE: Floppy disk  
1 COMPUTER: IBM PC compatible  
1 OPERATING SYSTEM: PC-DOS/MS-DOS  
1 SOFTWARE: PatentIn Release #1.0, Version #1.30  
1 CURRENT APPLICATION DATA:  
1 APPLICATION NUMBER: US/09/235,217  
1 FILING DATE:  
1 CLASSIFICATION:  
1 PRIOR APPLICATION DATA:  
1 APPLICATION NUMBER: US 08/480,473  
1 FILING DATE:  
1 ATTORNEY/AGENT INFORMATION:  
1 NAME: Haile, Lisa A.  
1 REGISTRATION NUMBER: 38,347  
1 REFERENCE/DOCKET NUMBER: 07265/053001  
1 TELECOMMUNICATION INFORMATION:  
1 TELEPHONE: 619/678-5070  
1 TELEFAX: 619/678-5099  
1 INFORMATION FOR SEQ ID NO: 1:  
1 SEQUENCE CHARACTERISTICS:  
1 LENGTH: 3736 base pairs  
1 TYPE: nucleic acid  
1 STRANDEDNESS: single  
1 TOPOLOGY: linear  
1 MOLECULE TYPE: DNA  
US-09-235-217-1

Query Match 92.0%; Score 18.4; DB 3; Length 3736;  
Best Local Similarity 95.0%; Pred. No. 6.8;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGCCAA 20  
DB 2555 AGTGAGCCACCAGTGCCAA 2536

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:21:21 ; Search time 823 Seconds  
(without alignments)  
298.606 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagccaccagtgtccaa 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18922170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA\_Main:\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	20	8	US-10-766-185-1
C 2	20	100.0	20	8	US-10-766-185-2
C 3	20	100.0	57500	9	US-10-719-370A-11
C 4	20	100.0	57501	8	US-10-304-126-11
C 5	19.6	100.0	1558	4	US-09-925-065A-706976
C 6	19.6	100.0	1558	5	US-09-925-065A-706976
C 7	18.4	92.0	37	6	US-10-190-394-2
C 8	18.4	92.0	375	8	US-10-242-535A-41677
C 9	18.4	92.0	375	8	US-10-085-783A-41677
C 10	18.4	92.0	1400	10	US-10-956-157-5878
C 11	18.4	92.0	2861	7	US-10-264-049-431
C 12	18.4	92.0	3180	7	US-10-425-784-3
C 13	18.4	92.0	3229	3	US-09-919-039-148
C 14	18.4	92.0	3229	6	US-10-208-408-22
C 15	18.4	92.0	3229	6	US-10-084-817-113
C 16	18.4	92.0	3229	7	US-10-247-671-19
C 17	18.4	92.0	3551	8	US-10-304-126-13

C 18	18.4	92.0	3551	9	US-10-719-370A-13	Sequence 13, Appl
C 19	18.4	92.0	3678	6	US-10-028-158-22	Sequence 22, Appl
C 20	18.4	92.0	3678	9	US-10-901-583-19	Sequence 19, Appl
C 21	18.4	92.0	3678	10	US-10-007-255-3	Sequence 3, Appl
C 22	18.4	92.0	3678	13	US-11-043-493-22	Sequence 22, Appl
C 23	18.4	92.0	3736	7	US-10-423-419-1	Sequence 1, Appl
C 24	18.4	92.0	3736	10	US-10-831-380-1	Sequence 3, Appl
C 25	18.4	92.0	3812	9	US-10-699-557-3	Sequence 21, Appl
C 26	18.4	92.0	3927	3	US-09-813-790-231	Sequence 3, Appl
C 27	18.4	92.0	3933	7	US-10-172-118-625	Sequence 231, App
C 28	18.4	92.0	3933	7	US-10-388-360-309	Sequence 625, App
C 29	18.4	92.0	3933	8	US-10-342-887-625	Sequence 309, App
C 30	18.4	92.0	3933	8	US-10-407-807-1	Sequence 625, App
C 31	18.4	92.0	3933	8	US-10-304-126-4	Sequence 1, Appl
C 32	18.4	92.0	3933	9	US-10-719-370A-4	Sequence 4, Appl
C 33	18.4	92.0	3933	9	US-10-719-370A-133	Sequence 4, Appl
C 34	18.4	92.0	3933	9	US-10-848-646-3	Sequence 133, App
C 35	18.4	92.0	3933	10	US-10-956-157-643	Sequence 3, Appl
C 36	18.4	92.0	3933	10	US-10-494-800-59	Sequence 643, App
C 37	18.4	92.0	3933	16	US-11-288-720-1	Sequence 59, Appl
C 38	18.4	92.0	3958	9	US-10-699-557-2	Sequence 2, Appl
C 39	18.4	92.0	4162	10	US-10-450-763-20862	Sequence 20862, A
C 40	18.4	92.0	4856	6	US-10-044-090-284	Sequence 284, App
C 41	18	90.0	20	9	US-10-719-370A-187	Sequence 187, App
C 42	18	90.0	3718	6	US-10-205-342-14	Sequence 14, Appl
C 43	18	90.0	3718	9	US-10-699-557-4	Sequence 4, Appl
C 44	18	90.0	3947	10	US-10-764-420-2663	Sequence 2663, Ap
C 45	18	90.0	3973	9	US-10-699-557-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-10-766-185-1/c

- Sequence 1, Application US/10766185
- Publication No. US20040152655A1
- GENERAL INFORMATION:
- APPLICANT: Yoon, Heejeong
- APPLICANT: Ahn, Chang Ho
- APPLICANT: Lee, Young Bok
- APPLICANT: Mao, Lingjun
- APPLICANT: Jiang, Xiaomeng
- TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
- FILE REFERENCE: REX 7034
- CURRENT APPLICATION NUMBER: US/10/766,185
- CURRENT FILING DATE: 2004-01-28
- NUMBER OF SEQ ID NOS: 130
- SOFTWARE: PatentIn version 3.1
- SEQ ID NO 1
- LENGTH: 20
- TYPE: DNA
- ORGANISM: human
- US-10-766-185-1

Query Match Best Local Similarity 100.0%; Score 20; DB 8; Length 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCAA 20

Db 20 AATGAGCCACCAGTGTCCAA 1

RESULT 2

US-10-766-185-2

- Sequence 2, Application US/10766185
- Publication No. US20040152655A1
- GENERAL INFORMATION:
- APPLICANT: Yoon, Heejeong
- APPLICANT: Ahn, Chang Ho
- APPLICANT: Lee, Young Bok
- APPLICANT: Mao, Lingjun



; APPLICANT: Jiang, Xiaoming  
; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIP-1  
; FILE REFERENCE: REX 7034  
; CURRENT APPLICATION NUMBER: US/10/766,185  
; CURRENT FILING DATE: 2004-01-28  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: antisense oligonucleotide  
US-10-766-185-2

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 20  
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Db 1 AATGAGCCACCAGTGTCCTCA 20

RESULT 3  
US-10-719-370A-11/c  
; Sequence 11, Application US/10/719370A  
; Publication No. US20040220393A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Donna T.  
; APPLICANT: Dobie, Kenneth W.  
; APPLICANT: Marcussen, Eric G.  
; APPLICANT: Freier, Susan M.  
; TITLE OF INVENTION: MODULATION OF HIF1A AND HIF2a EXPRESSION  
; FILE REFERENCE: ISPT-1010  
; CURRENT APPLICATION NUMBER: US/10/719,370A  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 10/304,126  
; PRIOR FILING DATE: 2002-11-23  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 11  
; LENGTH: 57500  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(57500)  
; OTHER INFORMATION: positions 82000 to 139500 of the sequence with GenBank Accession  
; PUBLICATION INFORMATION: ALI37129.4  
; DATABASE ENTRY DATE: 2001-04-30  
; RELEVANT RESIDUES: (1)..(57500)  
US-10-719-370A-11

Query Match 100.0%; Score 20; DB 9; Length 57500;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 20  
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Db 54374 AATGAGCCACCAGTGTCCTCA 54355

RESULT 4  
US-10-304-126-11/c  
; Sequence 11, Application US/10304126  
; Publication No. US20040101858A1  
; GENERAL INFORMATION:  
; APPLICANT: Donna T. Ward  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: MODULATION OF HYPOXIA-INDUCIBLE FACTOR 1 ALPHA EXPRESSION

; FILE REFERENCE: PTS-0070  
; CURRENT APPLICATION NUMBER: US/10/304,126  
; CURRENT FILING DATE: 2002-11-23  
; NUMBER OF SEQ ID NOS: 132  
; SEQ ID NO 11  
; LENGTH: 57501  
; TYPE: DNA  
; ORGANISM: H. sapiens  
US-10-304-126-11

Query Match 100.0%; Score 20; DB 8; Length 57501;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 54375 AATGAGCCACCAGTGTCCTCA 54356

RESULT 5  
US-09-925-065A-706976/c  
; Sequence 706976, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 706976  
; LENGTH: 1558  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-706976

Query Match 100.0%; Score 20; DB 4; Length 1558;  
Best Local Similarity 95.0%; Pred. No. 8.2;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 33 AATGAGCCACCAGTGTCCTCA 14

RESULT 6  
US-09-925-065A-706976/c  
; Sequence 706976, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 706976  
; LENGTH: 1558  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-706976

Query Match 100.0%; Score 20; DB 5; Length 1558;  
Best Local Similarity 95.0%; Pred. No. 8.2;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTAA 20  
|:|||||||||||||||||  
Db 33 ARTGAGCCACCAAGTGTCCTAA 14

## RESULT 7

US-10-190-394-2  
; Sequence 2, Application US/10190394  
; Publication No. US20030018007A1  
; GENERAL INFORMATION:  
; APPLICANT: Gregory, Richard  
; APPLICANT: Vincent, Karen  
; TITLE OF INVENTION: Compositions and Methods for Inducing Gene  
; FILE REFERENCE: Expression  
; CURRENT APPLICATION NUMBER: US/10/190,394  
; CURRENT FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US/09/579,897  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/067,546  
; PRIOR FILING DATE: 1997-12-04  
; PRIOR APPLICATION NUMBER: PCT/US98/25753  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: 09/133,612  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 37  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-190-394-2

Query Match 92.0%; Score 18.4; DB 6; Length 37;  
Best Local Similarity 95.0%; Pred. No. 29;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTAA 20  
|:|||||||||||||||||  
Db 8 AGTGAGCCACCAAGTGTCCTAA 27

## RESULT 8

US-10-242-535A-41677/c  
; Sequence 41677, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; APPLICANT: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 10/085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340

; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 41677  
; LENGTH: 375  
; TYPE: DNA  
; ORGANISM: Human  
US-10-242-535A-41677

Query Match 92.0%; Score 18.4; DB 8; Length 375;  
Best Local Similarity 95.0%; Pred. No. 32;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTAA 20  
|:|||||||||||||||||  
Db 165 AGTGAGCCACCAAGTGTCCTAA 146

## RESULT 9

US-10-085-783A-41677/c  
; Sequence 41677, Application US/10085783A  
; Publication No. US20040037841A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; APPLICANT: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2002  
; CURRENT APPLICATION NUMBER: US/10/085,783A  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 41677  
; LENGTH: 375  
; TYPE: DNA  
; ORGANISM: Human  
US-10-085-783A-41677

Query Match 92.0%; Score 18.4; DB 8; Length 375;  
Best Local Similarity 95.0%; Pred. No. 32;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAAGTGTCCTAA 20  
|:|||||||||||||||||  
Db 165 AGTGAGCCACCAAGTGTCCTAA 146

## RESULT 10

US-10-956-157-5878/c  
; Sequence 5878, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5878  
; LENGTH: 1400  
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-956-157-5878

Query Match          92.0%; Score 18.4; DB 10; Length 1400;
Best Local Similarity 95.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AATGAGCCACCAAGTGTCCTCA 20
Db      258 AGTGAGCCACCAAGTGTCCTCA 239

RESULT 11
US-10-264-049-431/c
; Sequence 431, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 431
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2853)..(2853)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-431

Query Match          92.0%; Score 18.4; DB 7; Length 2861;
Best Local Similarity 95.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AATGAGCCACCAAGTGTCCTCA 20
Db      1677 AGTGAGCCACCAAGTGTCCTCA 1658

RESULT 12
US-10-425-784-3/c
; Sequence 3, Application US/10425784
; Publication No. US20040009591A1
; GENERAL INFORMATION:
; APPLICANT: Comer, Allen
; APPLICANT: Hoffmann, Michael
; APPLICANT: Allen-Hoffmann, Lynn
; TITLE OF INVENTION: Keratinocytes Expressing Exogenous Angiogenic Growth Factors
; FILE REFERENCE: STRATA-08110
; CURRENT APPLICATION NUMBER: US/10/425,784
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 60/376,488
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 3180
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-425-784-3

Query Match          92.0%; Score 18.4; DB 7; Length 3180;
Best Local Similarity 95.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 AATGAGCCACCAAGTGTCCTCA 20
Db      2791 AGTGAGCCACCAAGTGTCCTCA 2772

RESULT 13
US-09-919-039-148/c
; Sequence 148, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 148
; LENGTH: 3229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1250434CBI
US-09-919-039-148

Query Match          92.0%; Score 18.4; DB 3; Length 3229;
Best Local Similarity 95.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AATGAGCCACCAAGTGTCCTCA 20
Db      2794 AGTGAGCCACCAAGTGTCCTCA 2775

RESULT 14
US-10-208-408-22/c
; Sequence 22, Application US/10208408
; Publication No. US20030096272A1
; GENERAL INFORMATION:
; APPLICANT: Schebye, Xiao Min
; TITLE OF INVENTION: GENES REGULATED BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR
; FILE REFERENCE: PA-0048-1 US
; CURRENT APPLICATION NUMBER: US/10/208,408
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,868
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 3229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030096272A1 1250434CBI
US-10-208-408-22

Query Match          92.0%; Score 18.4; DB 6; Length 3229;
Best Local Similarity 95.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AATGAGCCACCAAGTGTCCTCA 20
Db      2794 AGTGAGCCACCAAGTGTCCTCA 2775

RESULT 15
US-10-084-817-113/c
; Sequence 113, Application US/10084817
; Publication No. US20030119009A1
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; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 113
; LENGTH: 3229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 1250434CB1
US-10-084-817-113
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Query Match          92.0%; Score 18.4; DB 6; Length 3229;
Best Local Similarity 95.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AATGAGCCACCAGTGTCCAA 20
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Db      2794 AGTGAGCCACCAGTGTCCAA 2775
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Job time : 825 secs

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:33:45 ; Search time 13.5 Seconds  
(without alignments)  
104.527 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgagccaccagtgtccaa 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA\_New:\*\*

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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubna/US06\_NEW\_PUB.seq\*\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubna/US07\_NEW\_PUB.seq\*\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubna/US08\_NEW\_PUB.seq\*\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubna/PCT\_NEW\_PUB.seq\*\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubna/US10\_NEW\_PUB.seq\*\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubna/US11\_NEW\_PUB.seq\*\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubna/US60\_NEW\_PUB.seq\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.2	76.0	6327	7	US-11-217-529-75787 Sequence 75787, A
2	14.2	71.0	25	7	US-11-217-529-13735 Sequence 13735, A
3	14.2	71.0	163	7	US-11-301-554-1491 Sequence 1491, Ap
4	14.2	71.0	166	7	US-11-301-554-1393 Sequence 1393, Ap
5	14.2	71.0	166	7	US-11-301-554-1442 Sequence 1442, Ap
6	14.2	71.0	196	7	US-11-301-554-125 Sequence 125, App
7	14.2	71.0	422	7	US-11-301-554-1795 Sequence 1795, Ap
8	14.2	71.0	638	7	US-11-301-554-1283 Sequence 1283, Ap
9	14.2	71.0	663	7	US-11-217-529-710 Sequence 710, App
10	14.2	71.0	1041	7	US-11-301-924-21 Sequence 21, Appl
11	14.2	71.0	4600	7	US-11-301-554-1797 Sequence 1797, Ap
12	14.2	71.0	394191	6	US-10-506-549-3 Sequence 3, Appl
13	13.8	69.0	244	6	US-10-488-619-1090 Sequence 1090, Ap
14	13.8	69.0	2081	6	US-10-505-928-764 Sequence 764, App
15	13.8	69.0	3127	6	US-10-196-749-83 Sequence 83, Appl
16	13.8	69.0	17569	7	US-11-301-554-1804 Sequence 1804, Ap
17	13.6	68.0	192	7	US-11-217-529-174455 Sequence 174455, A
18	13.6	68.0	396	7	US-11-217-529-76998 Sequence 76998, A
19	13.6	68.0	438	6	US-11-217-529-78028 Sequence 78028, A
20	13.6	68.0	468	6	US-10-488-619-821 Sequence 821, App
21	13.6	68.0	711	7	US-11-217-529-4803 Sequence 4803, Ap
22	13.6	68.0	1446	7	US-11-217-529-76480 Sequence 76480, A
23	13.6	68.0	1506	7	US-11-217-529-81781 Sequence 81781, A
24	13.6	68.0	1749	7	US-11-217-529-2267 Sequence 2267, Ap
25	13.6	68.0	2379	7	US-11-217-529-79342 Sequence 79342, A

#### ALIGNMENTS

##### RESULT 1

US-11-217-529-75787  
; Sequence 75787, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 75787  
; LENGTH: 6327  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-75787

Query Match 76.0%; Score 15.2; DB 7; Length 6327;  
Best Local Similarity 85.0%; Pred. No. 19;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 AATGAGCCACCAGTGTCCAA 20

Db 2074 AAGGAGCTCCAGAGTCCAA 2093

##### RESULT 2

US-11-217-529-13735/c  
; Sequence 13735, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529

Sequence 616, App  
Sequence 533, App  
Sequence 2, Appli  
Sequence 37, Appl  
Sequence 490, App  
Sequence 79210, A  
Sequence 2765, Ap  
Sequence 80856, A  
Sequence 1, Appli  
Sequence 796, App  
Sequence 44186, A  
Sequence 86968, A  
Sequence 2733, Ap  
Sequence 4869, Ap  
Sequence 2902, Ap  
Sequence 1432, Ap  
Sequence 1993, Ap  
Sequence 2514, Ap  
Sequence 5849, Ap  
Sequence 2905, Ap

; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 13735  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-13735

Query Match 71.0%; Score 14.2; DB 7; Length 25;  
Best Local Similarity 84.2%; Pred. No. 21;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 19  
DB 24 ACTGAGCCGCCAGTGTCCTCA 6

## RESULT 3

US-11-301-554-1491  
; Sequence 1491, Application US/11301554  
; Publication No. US20060088527A1  
; GENERAL INFORMATION:

; APPLICANT: Henderson, Robert A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Johnson, Jeffrey C.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Durham, Margarita  
; APPLICANT: Carter, Darrick  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: McNabb, Andria  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.478C21  
; CURRENT APPLICATION NUMBER: US/11/301,554  
; CURRENT FILING DATE: 2005-12-13  
; PRIOR APPLICATION NUMBER: US 10/283,017  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US 10/113,872  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 10/017,754  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: US 09/902,941  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 09/849,626  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: US 09/736,457  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: US 09/702,705  
; PRIOR FILING DATE: 2000-10-30  
; PRIOR APPLICATION NUMBER: US 09/677,419  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: US 09/671,325  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/658,824  
; PRIOR FILING DATE: 2000-09-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 2157  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1491  
; LENGTH: 163  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-301-554-1491

Query Match 71.0%; Score 14.2; DB 7; Length 163;

Best Local Similarity 84.2%; Pred. No. 31;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 19  
DB 69 AACCTGCCACCAGTGTCCTCA 87

## RESULT 4

US-11-301-554-1393/c  
; Sequence 1393, Application US/11301554  
; Publication No. US20060088527A1  
; GENERAL INFORMATION:

; APPLICANT: Henderson, Robert A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Johnson, Jeffrey C.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Durham, Margarita  
; APPLICANT: Carter, Darrick  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: McNabb, Andria  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.478C21  
; CURRENT APPLICATION NUMBER: US/11/301,554  
; CURRENT FILING DATE: 2005-12-13  
; PRIOR APPLICATION NUMBER: US 10/283,017  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US 10/113,872  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 10/017,754  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: US 09/902,941  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 09/849,626  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: US 09/736,457  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: US 09/702,705  
; PRIOR FILING DATE: 2000-10-30  
; PRIOR APPLICATION NUMBER: US 09/677,419  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: US 09/671,325  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/658,824  
; PRIOR FILING DATE: 2000-09-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 2157  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1393  
; LENGTH: 166  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-301-554-1393

Query Match 71.0%; Score 14.2; DB 7; Length 166;  
Best Local Similarity 84.2%; Pred. No. 31;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 19  
DB 95 AACCTGCCACCAGTGTCCTCA 77

## RESULT 5

US-11-301-554-1442  
; Sequence 1442, Application US/11301554  
; Publication No. US20060088527A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Watanabe, Yoshihiro
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Sleath, Paul R.
/ APPLICANT: Johnson, Jeffrey C.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Durham, Margarita
/ APPLICANT: Carter, Darrick
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: McNabb, Andria
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C21
/ CURRENT APPLICATION NUMBER: US/11/301,554
/ CURRENT FILING DATE: 2005-12-13
/ PRIOR APPLICATION NUMBER: US 10/283,017
/ PRIOR FILING DATE: 2002-10-28
/ PRIOR APPLICATION NUMBER: US 10/113,872
/ PRIOR FILING DATE: 2002-03-28
/ PRIOR APPLICATION NUMBER: US 10/017,754
/ PRIOR FILING DATE: 2001-10-29
/ PRIOR APPLICATION NUMBER: US 09/902,941
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 09/849,626
/ PRIOR FILING DATE: 2001-05-03
/ PRIOR APPLICATION NUMBER: US 09/736,457
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: US 09/702,705
/ PRIOR FILING DATE: 2000-10-30
/ PRIOR APPLICATION NUMBER: US 09/677,419
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: US 09/671,325
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: US 09/658,824
/ PRIOR FILING DATE: 2000-09-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2157
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1442
/ LENGTH: 166
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-301-554-1442

Query Match 71.0%; Score 14.2; DB 7; Length 166;
Best Local Similarity 84.2%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 19
Db 72 AACCTGCCACCAGTGTCCTCA 90

RESULT 6
US-11-301-554-125
/ Sequence 125, Application US/11301554
/ Publication No. US20060088527A1
/ GENERAL INFORMATION:
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Watanabe, Yoshihiro
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Sleath, Paul R.
/ APPLICANT: Johnson, Jeffrey C.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Durham, Margarita
/ APPLICANT: Carter, Darrick
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: McNabb, Andria
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C21
/ CURRENT APPLICATION NUMBER: US/11/301,554
/ CURRENT FILING DATE: 2005-12-13
/ PRIOR APPLICATION NUMBER: US 10/283,017
/ PRIOR FILING DATE: 2002-10-28
/ PRIOR APPLICATION NUMBER: US 10/113,872
/ PRIOR FILING DATE: 2002-03-28
/ PRIOR APPLICATION NUMBER: US 10/017,754
/ PRIOR FILING DATE: 2001-10-29
/ PRIOR APPLICATION NUMBER: US 09/902,941
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 09/849,626
/ PRIOR FILING DATE: 2001-05-03
/ PRIOR APPLICATION NUMBER: US 09/736,457
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: US 09/702,705
/ PRIOR FILING DATE: 2000-10-30
/ PRIOR APPLICATION NUMBER: US 09/677,419
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: US 09/671,325
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: US 09/658,824
/ PRIOR FILING DATE: 2000-09-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2157
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1442
/ LENGTH: 166
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-301-554-1442
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/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: McNabb, Andria
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C21
/ CURRENT APPLICATION NUMBER: US/11/301,554
/ CURRENT FILING DATE: 2005-12-13
/ PRIOR APPLICATION NUMBER: US 10/283,017
/ PRIOR FILING DATE: 2002-10-28
/ PRIOR APPLICATION NUMBER: US 10/113,872
/ PRIOR FILING DATE: 2002-03-28
/ PRIOR APPLICATION NUMBER: US 10/017,754
/ PRIOR FILING DATE: 2001-10-29
/ PRIOR APPLICATION NUMBER: US 09/902,941
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 09/849,626
/ PRIOR FILING DATE: 2001-05-03
/ PRIOR APPLICATION NUMBER: US 09/736,457
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: US 09/702,705
/ PRIOR FILING DATE: 2000-10-30
/ PRIOR APPLICATION NUMBER: US 09/677,419
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: US 09/671,325
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: US 09/658,824
/ PRIOR FILING DATE: 2000-09-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2157
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 125
/ LENGTH: 196
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-301-554-125

Query Match 71.0%; Score 14.2; DB 7; Length 196;
Best Local Similarity 84.2%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCAGTGTCCTCA 19
Db 102 AACCTGCCACCAGTGTCCTCA 120

RESULT 7
US-11-301-554-1795/c
/ Sequence 1795, Application US/11301554
/ Publication No. US20060088527A1
/ GENERAL INFORMATION:
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Watanabe, Yoshihiro
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Sleath, Paul R.
/ APPLICANT: Johnson, Jeffrey C.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Durham, Margarita
/ APPLICANT: Carter, Darrick
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: McNabb, Andria
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C21
/ CURRENT APPLICATION NUMBER: US/11/301,554
/ CURRENT FILING DATE: 2005-12-13
/ PRIOR APPLICATION NUMBER: US 10/283,017
/ PRIOR FILING DATE: 2002-10-28
/ PRIOR APPLICATION NUMBER: US 10/113,872
/ PRIOR FILING DATE: 2002-03-28
/ PRIOR APPLICATION NUMBER: US 10/017,754
/ PRIOR FILING DATE: 2001-10-29
/ PRIOR APPLICATION NUMBER: US 09/902,941
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 09/849,626
/ PRIOR FILING DATE: 2001-05-03
/ PRIOR APPLICATION NUMBER: US 09/736,457
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: US 09/702,705
/ PRIOR FILING DATE: 2000-10-30
/ PRIOR APPLICATION NUMBER: US 09/677,419
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: US 09/671,325
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: US 09/658,824
/ PRIOR FILING DATE: 2000-09-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2157
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 125
/ LENGTH: 196
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-301-554-125
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; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1795
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 295, 378, 390
; OTHER INFORMATION: n = A,T,C or G
US-11-301-554-1795

Query Match      71.0%; Score 14.2; DB 7; Length 422;
Best Local Similarity 84.2%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AATGAGCCACCAAGTGTCCTCA 19
Db      130 AACCTGCCACCAAGTGTCCTCA 112

RESULT 8
US-11-301-554-1283/c
; Sequence 1283, Application US/11301554
; Publication No. US2006098527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongcong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kales, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705

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; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1283
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-1283

Query Match      71.0%; Score 14.2; DB 7; Length 638;
Best Local Similarity 84.2%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AATGAGCCACCAAGTGTCCTCA 19
Db      389 AACCTGCCACCAAGTGTCCTCA 371

RESULT 9
US-11-217-529-710/c
; Sequence 710, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 710
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-710

Query Match      71.0%; Score 14.2; DB 7; Length 663;
Best Local Similarity 84.2%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AATGAGCCACCAAGTGTCCTCA 19
Db      316 ACTGAGCCGCCACCAAGTGTCCTCA 298

RESULT 10
US-11-301-924-21
; Sequence 21, Application US/11301924
; Publication No. US20060090218A1
; GENERAL INFORMATION:
; APPLICANT: Joshua Z. Levin
; APPLICANT: Ken Phillips
; APPLICANT: Greg Budziszewski
; APPLICANT: Fred Meins
; APPLICANT: Zhenya Glazov
; TITLE OF INVENTION: Methods of Controlling Gene Expression
; FILE REFERENCE: 31481USNP
; CURRENT APPLICATION NUMBER: US/11/301,924
; CURRENT FILING DATE: 2005-12-13

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;; PRIOR APPLICATION NUMBER: US/09/896,186  
;; PRIOR FILING DATE: 2001-06-29  
;; PRIOR APPLICATION NUMBER: 60/222,202  
;; PRIOR FILING DATE: 2000-08-01  
;; NUMBER OF SEQ ID NOS: 34  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 21  
;; LENGTH: 1041  
;; TYPE: DNA  
;; ORGANISM: Arabidopsis thaliana  
US-11-301-924-21

Query Match 71.0%; Score 14.2; DB 7; Length 1041;  
Best Local Similarity 84.2%; Pred. No. 45;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCCA 19  
|||  
DB 49 AATGAGCCACCACTGTCCGA 67

## RESULT 11

US-11-301-554-1797  
;; Sequence 1797, Application US/11301554  
;; Publication No. US20060088527A1  
;; GENERAL INFORMATION:

;; APPLICANT: Henderson, Robert A.  
;; APPLICANT: Wang, Tongtong  
;; APPLICANT: Watanabe, Yoshihiro  
;; APPLICANT: Kalos, Michael D.  
;; APPLICANT: Sleath, Paul R.  
;; APPLICANT: Johnson, Jeffrey C.  
;; APPLICANT: Retter, Marc W.  
;; APPLICANT: Durham, Margarita  
;; APPLICANT: Carter, Derrick  
;; APPLICANT: Fanger, Gary R.  
;; APPLICANT: Vedvick, Thomas S.  
;; APPLICANT: Bangur, Chaitanya S.  
;; APPLICANT: McNabb, Andria

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
;; OF LUNG CANCER

;; FILE REFERENCE: 210121.478C21  
;; CURRENT APPLICATION NUMBER: US/11/301,554  
;; CURRENT FILING DATE: 2005-12-13  
;; PRIOR APPLICATION NUMBER: US 10/283,017  
;; PRIOR FILING DATE: 2002-10-28  
;; PRIOR APPLICATION NUMBER: US 10/113,872  
;; PRIOR FILING DATE: 2002-03-28  
;; PRIOR APPLICATION NUMBER: US 10/017,754  
;; PRIOR FILING DATE: 2001-10-29  
;; PRIOR APPLICATION NUMBER: US 09/902,941  
;; PRIOR FILING DATE: 2001-07-10  
;; PRIOR APPLICATION NUMBER: US 09/849,626  
;; PRIOR FILING DATE: 2001-05-03  
;; PRIOR APPLICATION NUMBER: US 09/736,457  
;; PRIOR FILING DATE: 2000-12-13  
;; PRIOR APPLICATION NUMBER: US 09/702,705  
;; PRIOR FILING DATE: 2000-10-30  
;; PRIOR APPLICATION NUMBER: US 09/677,419  
;; PRIOR FILING DATE: 2000-10-06  
;; PRIOR APPLICATION NUMBER: US 09/671,325  
;; PRIOR FILING DATE: 2000-09-26  
;; PRIOR APPLICATION NUMBER: US 09/658,824  
;; PRIOR FILING DATE: 2000-09-08

;; Remaining Prior Application data removed - See File Wrapper or PALM.

;; NUMBER OF SEQ ID NOS: 2157  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1797  
;; LENGTH: 4600  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-11-301-554-1797

Query Match 71.0%; Score 14.2; DB 7; Length 4600;  
Best Local Similarity 84.2%; Pred. No. 61;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGAGCCACCACTGTCCCA 19  
|||  
DB 3767 AACTGTCCACCACTGTCCCA 3785

## RESULT 12

US-10-506-549-3/c  
;; Sequence 3, Application US/10506549  
;; Publication No. US20060100417A1  
;; GENERAL INFORMATION:

;; APPLICANT: APPLERA CORPORATION  
;; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
;; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
;; TITLE OF INVENTION: AND USES THEREOF  
;; FILE REFERENCE: CL001361-US

;; CURRENT APPLICATION NUMBER: US/10/506,549

;; CURRENT FILING DATE: 2004-09-03

;; PRIOR APPLICATION NUMBER: 60/361,343

;; PRIOR FILING DATE: 2002-03-05

;; NUMBER OF SEQ ID NOS: 4

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 3

;; LENGTH: 394191

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: misc\_feature

;; LOCATION: (1)..(394191)

;; OTHER INFORMATION: n = A,T,C or G

US-10-506-549-3

Query Match 71.0%; Score 14.2; DB 6; Length 394191;

Best Local Similarity 84.2%; Pred. No. 1e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGAGCCACCACTGTCCAA 20  
|||  
DB 130263 ATGAGCCACCACTGTCCAA 130245

## RESULT 13

US-10-488-619-1090

;; Sequence 1090, Application US/10488619

;; Publication No. US20060099578A1

;; GENERAL INFORMATION:

;; APPLICANT: Greenlee, Winner and Sullivan, P.C.

;; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
;; OF Physiological Conditions, And Genotyping Arrays

;; FILE REFERENCE: 98-01 WO

;; CURRENT APPLICATION NUMBER: US/10/488,619

;; CURRENT FILING DATE: 2004-03-01

;; NUMBER OF SEQ ID NOS: 3040

;; SOFTWARE: PatentIn version 3.1

;; SEQ ID NO 1090

;; LENGTH: 244

;; TYPE: DNA

;; ORGANISM: Mus musculus

US-10-488-619-1090

Query Match 69.0%; Score 13.8; DB 6; Length 244;

Best Local Similarity 88.2%; Pred. No. 55;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGCCACCACTGTCCCA 19  
|||  
DB 95 TGAGCCACCACTGTCCCA 111

## RESULT 14

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US-10-505-928-764
; Sequence 764, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 764
; LENGTH: 2081
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-764

Query Match      69.0%; Score 13.8; DB 6; Length 2081;
Best Local Similarity 88.2%; Pred. No. 84;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3  TGAGCCACCAGTGTCCTCA 19
      ||||| ||||| |||||
Db      1596 TGAGCAACCACTGTCTCA 1612

RESULT 15
US-10-196-749-83/c
; Sequence 83, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 83
; LENGTH: 3127

; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-83

Query Match      69.0%; Score 13.8; DB 6; Length 3127;
Best Local Similarity 88.2%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  GAGCCACCAGTGTCCTCA 20
      ||||| ||||| |||||
Db      1417 GTGCCACGAGTGTCCTCA 1401

Search completed: May 21, 2006, 21:34:21
Job time : 14.5 secs
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:34:32 ; Search time 1030.5 Seconds  
(without alignments)  
1241.095 Million cell updates/sec

Title: US-10-766-185-4  
Perfect score: 20  
Sequence: 1 ggagctaacatctccaagtc 20  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues  
Total number of hits satisfying chosen parameters: 2296392

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_env.\*  
2: gb\_pat.\*  
3: gb\_pl.\*  
4: gb\_pl.\*  
5: gb\_pr.\*  
6: gb\_ro.\*  
7: gb\_ats.\*  
8: gb\_ey.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	49	2	BD187062	Polypepti
2	16	80.0	16	2	AX927927	Sequence
3	15.2	76.0	21	2	DD159257	Primer fo
4	14	70.0	49	2	BD187064	Polypepti
5	13.6	68.0	40	2	AR119846	Sequence
6	13.6	68.0	40	2	AX077752	Sequence
7	13.6	68.0	41	2	AR119858	Sequence
8	13.6	68.0	41	2	AX077751	Sequence
9	13.6	68.0	41	2	AX518106	Sequence
10	13.6	68.0	42	2	AR119859	Sequence
11	13.6	68.0	42	2	AX224363	Sequence
12	13.4	67.0	20	2	AR312573	Sequence
13	13.4	67.0	27	2	A25211	inter-Alu s
14	13.4	67.0	27	2	E09139	Synthetic D
15	13	65.0	28	2	A24719	primer 2065
16	13	65.0	28	2	A24722	primer 2070
17	12.8	64.0	24	2	AR640085	Sequence
18	12.8	64.0	24	2	AR640086	Sequence

C	19	12.8	64.0	24	2	AX544252	Sequence
C	20	12.8	64.0	24	2	AX544253	Sequence
C	21	12.8	64.0	29	2	AR561068	Sequence
C	22	12.8	64.0	38	2	CO801003	Sequence
C	23	12.8	64.0	47	2	AR290208	Sequence
C	24	12.8	64.0	50	2	AR685481	Sequence
C	25	12.6	63.0	21	2	AR531344	Sequence
C	26	12.6	63.0	21	2	AX097369	Sequence
C	27	12.6	63.0	26	2	AR119845	Sequence
C	28	12.6	63.0	27	2	DD187294	Sequence
C	29	12.6	63.0	30	2	DD187291	Sequence
C	30	12.6	63.0	38	2	AR287012	Sequence
C	31	12.6	63.0	38	2	AR399002	Sequence
C	32	12.6	63.0	39	2	AR1014283	Sequence
C	33	12.6	63.0	39	2	AR103038	Sequence
C	34	12.6	63.0	39	2	AR364199	Sequence
C	35	12.4	62.0	20	2	AR067326	Sequence
C	36	12.4	62.0	20	2	CS145074	Sequence
C	37	12.4	62.0	27	2	BD103613	Peptide a
C	38	12.4	62.0	27	2	BD103615	Peptide a
C	39	12.4	62.0	27	2	BD103617	Peptide a
C	40	12.4	62.0	27	2	BD103620	Peptide a
C	41	12.4	62.0	27	2	DD165976	Mutains o
C	42	12.4	62.0	27	2	DD165977	Mutains o
C	43	12.4	62.0	27	2	AR577077	Sequence
C	44	12.4	62.0	27	2	AR577079	Sequence
C	45	12.4	62.0	27	2	AR577081	Sequence

ALIGNMENTS

RESULT 1	BD187062	49 bp	DNA	linear	PAT 17-JUN-2003
LOCUS	Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.				
DEFINITION	Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.				
ACCESSION	BD187062				
VERSION	BD187062.1 GI:31879262				
KEYWORDS	WO 02099104-A/22.				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1 (bases 1 to 49)				
AUTHORS	Hiraoka, M., Kondo, S. and Harada, H.				
TITLE	Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it				
JOURNAL	Patent: WO 02099104-A 22 12-DEC-2002; POLA CHEMICAL INDUSTRIES INC, MASAHIRO HIRAOKA, SHINAE KONDO, HIROSHI HARADA				
COMMENT	OS Artificial Sequence PN WO 02099104-A/22 PD 13-DEC-2002 PF 04-JUN-2002 WO 2002JP005482 PR 05-JUN-2001 JP 01P 169948, 05-JUN-2001 JP 01P 169949 PI MASAHIRO HIRAOKA, SHINAE KONDO, HIROSHI HARADA PC C12N15/09, C12Q1/68, C07K14/47, C07K19/00 CC Description of Artificial Sequence: synthetic DNA FH Key Location/Qualifiers FT source 1..49 FT /organism='Artificial Sequence'. Location/Qualifiers 1..49 /organism='synthetic construct' /mol_type='genomic DNA' /db_xref='taxon:32630'				
FEATURES	source				
ORIGIN					
Query Match	100.0%;	Score 20;	DB 2;	Length 49;	
Best Local Similarity	100.0%;	Pred. No. 17;			
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GGAGCTACATCTCCCAAGTC	20		

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Db      26 GGAGCTAACATCTCCCAAGTC 45
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RESULT 2
AX927927
LOCUS      16 bp      DNA      linear      PAT 19-DEC-2003
DEFINITION Sequence 13 from Patent WO03085110.
ACCESSION AX927927
VERSION    AX927927.1 GI:40250734
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE 1
AUTHORS    Thru, C.A., h G.A.M. and Kristjansen, P.E.
TITLE      Oligomeric compounds for the modulation hlf-lalpha expression
JOURNAL    Patent: WO 03085110-A 13 16-OCT-2003;
           Cureon A/S (DK)
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
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ORIGIN
Query Match      80.0%; Score 16; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GCTAACATCTCCCAAGT 19
|||||
Db      1 GCTAACATCTCCCAAGT 16

RESULT 3
DD159257
LOCUS      21 bp      DNA      linear      PAT 23-NOV-2005
DEFINITION Primer for detecting human enterobacteria.
ACCESSION DD159257
VERSION    DD159257.1 GI:83957554
KEYWORDS   JP 2005124495-A/33.
SOURCE     unidentified
ORGANISM   unclassified sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS    Watanabe, K., Fujimoto, J. and Matsuki, T.
TITLE      Primer for detecting human enterobacteria
JOURNAL    Patent: JP 2005124495-A 33 19-MAY-2005;
           KABUSHIKI KAISHA YAKULT HONSHA
COMMENT    OS Designed primer based on 16SrRNA of human enterobacteria PN
           JP 2005124495-A/33
           PD 19-MAY-2005
           PF 24-OCT-2003 JP 2003364188
           PI koichi watanabe, junji fujimoto, takahiro matsuki CC
           FH Key Location/Qualifiers
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            /db_xref="taxon:32644"
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Query Match      76.0%; Score 15.2; DB 2; Length 21;
Best Local Similarity 85.0%; Pred. No. 5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGAGCTAACATCTCCCAAGTC 20
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Db      2 GGAGCTTGCTTCTCCCAAGTC 21
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Db      26 GGAGCTAACATCTCCCAAGTC 45
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RESULT 4
BD187064
LOCUS      49 bp      DNA      linear      PAT 17-JUN-2003
DEFINITION Polypeptide causing protein unstable in cell under aerobic
           condition and DNA encoding it.
ACCESSION BD187064
VERSION    BD187064.1 GI:31879264
KEYWORDS   WO 02099104-A/24.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 49)
AUTHORS    Hiraoka, M., Kondo, S. and Harada, H.
TITLE      Polypeptide causing protein unstable in cell under aerobic
           condition and DNA encoding it
JOURNAL    Patent: WO 02099104-A 24 12-DEC-2002;
           POLA CHEMICAL INDUSTRIES INC, MASAHIRO HIRAOKA, SHINAE KONDO, HIROSHI
           HARADA
COMMENT    OS Artificial Sequence
           PN WO 02099104-A/24
           PD 12-DEC-2002
           PF 04-JUN-2002 WO 2002JP005482
           PR 05-JUN-2001 JP 01P 169948, 05-JUN-2001 JP 01P 169949 PI
           MASASHIRO HIRAOKA, SHINAE KONDO, HIROSHI HARADA
           PC C12N15/09, C12Q1/68, C07K14/47, C07K19/00
           CC Description of Artificial Sequence: synthetic DNA FH Key
           Location/Qualifiers
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           1..49
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ORIGIN
Query Match      70.0%; Score 14; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGAGCTAACATCTC 14
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Db      35 GGAGCTAACATCTC 48
|||||

RESULT 5
AR119846/c
LOCUS      40 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 19 from patent US 6153421.
ACCESSION AR119846
VERSION    AR119846.1 GI:14102545
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE 1 (bases 1 to 40)
AUTHORS    Yanagi, M., Bukh, J., Emerson, S.U. and Purcell, R.H.
TITLE      Cloned genomes of infectious hepatitis C viruses and uses thereof
JOURNAL    Patent: US 6153421-A 19 28-NOV-2000;
           Location/Qualifiers
FEATURES   Location/Qualifiers
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            1..40
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ORIGIN
Query Match      68.0%; Score 13.6; DB 2; Length 40;
Best Local Similarity 80.0%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGAGCTAACATCTCCCAAGTC 20
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Db      33 GGAGCTAACCACTCCAGGCC 14
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RESULT 6  
 AX077752/c  
 LOCUS AX077752 40 bp DNA linear PAT 22-FEB-2001  
 DEFINITION Sequence 18 from Patent WO0106008.  
 ACCESSION AX077752  
 VERSION AX077752.1 GI:13157648  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Singh, S., Inamdar, A., Ullman, E.F., Cao, L. and Albagli, D.  
 TITLE Multiplexed strand displacement for nucleic acid determinations  
 JOURNAL Patent: WO 0106008-A 18 25-JAN-2001;  
 Aclara Biosciences, Inc. (US)  
 FEATURES  
 source 1. .40  
 /organism="synthetic construct"  
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 /db\_xref="taxon:32630"  
 /note="probe"  
 ORIGIN  
 Query Match 68.0%; Score 13.6; DB 2; Length 40;  
 Best Local Similarity 80.0%; Pred. No. 4e+04; Mismatches 4; Indels 0; Gaps 0;  
 Matches 16; Conservative 0;  
 QY 1 GGAGCTAACATCTCCAAAGTC 20  
 |||||  
 Db 26 GGACCTCAGCTCTCAAGTC 7  
 |||||  
 RESULT 7  
 AR119858  
 LOCUS AR119858 41 bp DNA linear PAT 16-MAY-2001  
 DEFINITION Sequence 50 from patent US 6153421.  
 ACCESSION AR119858  
 VERSION AR119858.1 GI:14102557  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 41)  
 AUTHORS Yanagi, M., Bukh, J., Emerson, S.U. and Purcell, R.H.  
 TITLE Cloned genomes of infectious hepatitis C viruses and uses thereof  
 JOURNAL Patent: US 6153421-A 50 28-NOV-2000;  
 FEATURES  
 source 1. .41  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 ORIGIN  
 Query Match 68.0%; Score 13.6; DB 2; Length 41;  
 Best Local Similarity 80.0%; Pred. No. 4e+04; Mismatches 4; Indels 0; Gaps 0;  
 Matches 16; Conservative 0;  
 QY 1 GGAGCTAACATCTCCAAAGTC 20  
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 Db 8 GGAGCTAACATCTCCAGGCC 27  
 |||||  
 RESULT 8  
 AX077751  
 LOCUS AX077751 41 bp DNA linear PAT 22-FEB-2001  
 DEFINITION Sequence 17 from Patent WO0106008.  
 ACCESSION AX077751  
 VERSION AX077751.1 GI:13157647  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Singh, S., Inamdar, A., Ullman, E.F., Cao, L. and Albagli, D.  
 TITLE Multiplexed strand displacement for nucleic acid determinations  
 JOURNAL Patent: WO 0106008-A 17 25-JAN-2001;  
 Aclara Biosciences, Inc. (US)  
 FEATURES  
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 /db\_xref="taxon:32630"  
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 probe"  
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 Best Local Similarity 80.0%; Pred. No. 4e+04; Mismatches 4; Indels 0; Gaps 0;  
 Matches 16; Conservative 0;  
 QY 1 GGAGCTAACATCTCCAAAGTC 20  
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 Db 16 GGACCTCAGCTCTCAAGTC 35  
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 RESULT 9  
 AX518106/c  
 LOCUS AX518106 41 bp DNA linear PAT 05-OCT-2002  
 DEFINITION Sequence 4304 from Patent WO02052044.  
 ACCESSION AX518106  
 VERSION AX518106.1 GI:23567425  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 REFERENCE 1  
 AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
 TITLE Detection of genetic polymorphisms  
 JOURNAL Patent: WO 02052044-A 4304 04-JUL-2002;  
 Riken (JP)  
 FEATURES  
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 Best Local Similarity 80.0%; Pred. No. 4e+04; Mismatches 4; Indels 0; Gaps 0;  
 Matches 16; Conservative 0;  
 QY 1 GGAGCTAACATCTCCAAAGTC 20  
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 Db 27 GAAGCTYAAGTCTCCAAAGTC 8  
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 RESULT 10  
 AR119859  
 LOCUS AR119859 42 bp DNA linear PAT 16-MAY-2001  
 DEFINITION Sequence 51 from patent US 6153421.  
 ACCESSION AR119859  
 VERSION AR119859.1 GI:14102558  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 42)  
 AUTHORS Yanagi, M., Bukh, J., Emerson, S.U. and Purcell, R.H.  
 TITLE Cloned genomes of infectious hepatitis C viruses and uses thereof  
 JOURNAL Patent: US 6153421-A 51 28-NOV-2000;  
 FEATURES  
 source 1. .42  
 /organism="Homo sapiens"  
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/mol_type="unassigned DNA"

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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 8 GGAGCTAACCACTCCAGGCC 27

RESULT 11
AX224363
LOCUS AX224363 42 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 7 from Patent WO0161041.
ACCESSION AX224363
VERSION AX224363.1 GI:15554615
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Sharat,S., Cao,L., Hooper,H.H., Albagli,D., Anderson,R. and Zeng,S.
TITLE Multiple-site reaction device and method
JOURNAL Patent: WO 0161041-A 7 23-AUG-2001;
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/notes="n = triethyleneglycl"
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Best Local Similarity 68.0%; Score 13.6; DB 2; Length 42;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 15 GGACCTCAGCTTACAAGTC 34

RESULT 12
AR312573
LOCUS AR312573 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3110 from patent US 6559294.
ACCESSION AR312573
VERSION AR312573.1 GI:31705999
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffiths,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 3110 06-MAY-2003;
FEATURES
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source Location/Qualifiers
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ORIGIN
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Best Local Similarity 67.0%; Score 13.4; DB 2; Length 20;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGCTAACATCTCCAAGTC 20
Db 20 GAGCYRAGATCTCGAGTC 2

RESULT 14
E09139/c
LOCUS E09139 27 bp DNA linear PAT 29-SEP-1997
DEFINITION Synthetic DNA for Alu specific primer.
ACCESSION E09139
VERSION E09139.1 GI:22025765
KEYWORDS JP 1995115999-A/2.
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Ando,asu,H.A. and Yan,P.
TITLE DETECTING METHOD FOR DNA ARRANGEMENT VARIATION
JOURNAL Patent: JP 1995115999-A 2 09-MAY-1995;
COMMENT INGENII BV
OS None
OC Artificial sequences.
PN JP 1995115999-A/2
PD 09-MAY-1995
PF 22-MAY-1992 JP 1992130668
PI ANDO,ASU HERARUDOSU AITSUTERURINDEN, YAN FUEIKU PC
CC C12Q1/68,C12N15/00,G01N27/447,G01N27/447;
CC strandedness: Single;
CC topology: Linear;
FH key Location/Qualifiers
FT source 1..27
FT misc_feature 1..27
FT note="Alu specific primer".
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source Location/Qualifiers
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ORIGIN

Query Match 67.0%; Score 13.4; DB 2; Length 27;  
 Best Local Similarity 73.7%; Pred. No. 4.7e+04;  
 Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAAAGTC 20  
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 Db 20 GAGCYRAGATCTGAGGTC 2

RESULT 15

A24719/c 28 bp DNA linear PAT 24-JAN-1995  
 LOCUS A24719  
 DEFINITION primer 2065.  
 ACCESSION A24719  
 VERSION A24719.1 GI:833452  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 28)  
 AUTHORS Little, S., Ferris, R.M. and Robertson, N.H.  
 TITLE Detection method for nucleotide sequences  
 JOURNAL Patent: EP 0497527-A 71 05-AUG-1992;  
 IMPERIAL CHEMICAL INDUSTRIES PLC; ZENECA LIMITED  
 FEATURES  
 source  
 1..28  
 Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
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ORIGIN

Query Match 65.0%; Score 13; DB 2; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AACATCTCCAAGT 19  
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 Db 27 AACATCTCCAAGT 15

Search completed: May 21, 2006, 22:09:02  
 Job time : 1032.5 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:34:08 ; Search time 386 Seconds  
(without alignments)  
361.256 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggagctaacatctccaagtc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5218826

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_8:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
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6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*  
14: Geneseqn2005s:\*  
15: Geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	20	13	ADQ88723
2	20	100.0	20	13	ADQ88724
3	20	100.0	49	8	ABZ76611
4	16	80.0	16	10	AA156916
5	15.2	76.0	21	14	AA15801
6	14.2	71.0	26	14	AEC27934
7	14.2	71.0	26	14	AEC25568
8	14.2	71.0	30	12	ADQ31421
9	14	70.0	49	8	ABZ76613
C 10	13.8	69.0	25	9	AC111456
11	13.8	69.0	36	14	AED66358
12	13.8	69.0	36	14	AED66354
13	13.8	69.0	41	6	ABZ23749
14	13.8	69.0	41	6	ABZ23750
C 15	13.6	68.0	27	12	ADQ31172
16	13.6	68.0	30	3	AA176302
C 17	13.6	68.0	40	2	AA124853
18	13.6	68.0	40	5	AAF30251

C	19	13.6	68.0	40	5	AAF30252	Aaf30252 Dystrophin
	20	13.6	68.0	41	2	AAX24837	Aax24837 Infectiou
C	21	13.6	68.0	41	6	ABZ47520	Abz47520 Human ATP
	22	13.6	68.0	41	8	ACC59493	Acc59493 Multiple
	23	13.6	68.0	42	2	AAX24838	Aax24838 Infectiou
	24	13.6	68.0	42	5	AAS11922	Aas11922 Duplex fo
	25	13.4	67.0	20	2	AAX93784	Aax93784 PCR prime
C	26	13.4	67.0	27	2	AAQ33142	AAQ33142 Inter-Alu
	27	13.4	67.0	29	10	ADG87085	Adg87085 Light cha
	28	13.4	67.0	47	10	ADG87088	Adg87088 Light cha
C	29	13.2	66.0	21	7	ADJ78661	Adj78661 Pancreat
	30	13.2	66.0	28	12	ADN27437	Adn27437 CFTR gene
	31	13.2	66.0	28	12	ADO50557	ADO50557 CFTR inva
	32	13.2	66.0	28	12	ADO31715	ADO31715 Human CFT
C	33	13	65.0	21	4	AAF97782	Aaf97782 Human gen
C	34	13	65.0	28	2	AAQ26890	Aaq26890 Primer 20
C	35	13	65.0	28	2	AAQ26893	Aaq26893 Primer 20
C	36	12.8	64.0	18	14	AEC49071	Aec49071 Antisense
C	37	12.8	64.0	18	14	AEC49165	Aec49165 Antisense
C	38	12.8	64.0	20	10	ABZ97442	Abz97442 Human IL4
C	39	12.8	64.0	20	11	ABD30473	Abd30473 Human IL4
C	40	12.8	64.0	20	12	ADJ59261	Adj59261 Oligonucle
C	41	12.8	64.0	20	12	ADO44751	Ado44751 Human oli
C	42	12.8	64.0	21	13	ADU40891	Adu40891 Knock-down
C	43	12.8	64.0	24	6	ABT05788	Abt05788 Nod2 rela
C	44	12.8	64.0	24	6	ABT05789	Abt05789 Nod2 rela
	45	12.8	64.0	26	12	ADQ35304	Adq35304 Cardiomyo

#### ALIGNMENTS

RESULT 1  
ADQ88723/c  
ID ADQ88723 standard; DNA; 20 BP.

XX ADQ88723;

DT 21-OCT-2004 (first entry)

DE Human hypoxia inducible factor-1 gene fragment seqid 2.

KW RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;  
cancer; infection; inflammation; tumour formation; ss.

XX Homo sapiens.

PN US2004152655-A1.

PD 05-AUG-2004.

PF 28-JAN-2004; 2004US-00766185.

PR 31-JAN-2003; 2003US-0444367P.

XX (YOON/) YOON H.

PA (MAOL/) MAO L.

PA (LEHY/) LEE Y B.

PA (AHNC/) AHN C.

XX (JIAN/) JIANG X.

XX Yoon H, Mao L, Lee YB, Ahn C, Jiang X;

DR WPI; 2004-561492/54.

XX New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a  
PT nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),  
PT useful for inhibiting expression of HIF-1 and inducing cytotoxicity in  
PT several cancer cells.

XX Example 4; SEQ ID NO 3; 35pp; English.

CC The invention describes a compound, RX-0047 or RX-0149 targeted to a



CC nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),  
 CC where the oligonucleotide compound inhibits the expression of human HIF-  
 CC 1. Also described are: a method of inhibiting the expression of HIF-1 in  
 CC human cells or tissues; and a method of inducing cytotoxicity in a cancer  
 CC cell. Specifically claimed are RX-0047 and RX-0149 compounds having a  
 CC fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5'  
 CC atgagccaccagtgtccaa 3' and SEQ ID NO. 4, 5' ggagctaacatctccaagtc 3',  
 CC respectively). The compounds are useful for inhibiting the expression of  
 CC HIF-1 and inducing the cytotoxicity in several cancer cells. The  
 CC antisense compounds are also useful for preventing or delaying infection,  
 CC inflammation, or tumour formation. This sequence represents a site on the  
 CC HIF-1 to which antisense oligonucleotides can be targeted in order to  
 CC control HIF-1 gene expression.

XX SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 13; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.7; Indels 0; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 0;

QY 1 GGAGCTAACATCTCCAAGTC 20  
 DB 20 GGAGCTAACATCTCCAAGTC 1

RESULT 2  
 ADQ88724  
 ID ADQ88724 standard; DNA; 20 BP.  
 XX AC ADQ88724;  
 XX DT 21-OCT-2004 (first entry)  
 XX DE Human HIF-1 antisense oligonucleotide RX-0149.  
 XX KW RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;  
 XX cancer; infection; inflammation; tumour formation; ss;  
 XX antisense oligonucleotide; antisense technology.

OS Homo sapiens.  
 XX US2004152655-A1.  
 XX PD 05-AUG-2004.  
 XX PF 28-JAN-2004; 2004US-00766185.  
 XX PR 31-JAN-2003; 2003US-0444367P.

XX (YOON/) YOON H.  
 XX PA (MAOL/) MAO L.  
 XX PA (LEHY/) LEE Y B.  
 XX PA (AHNG/) AHN C.  
 XX PA (JIAN/) JIANG X.  
 XX PI Yoon H, Mao L, Lee YB, Ahn C, Jiang X;  
 XX DR WPI; 2004-561492/54.

XX New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a  
 PT nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),  
 PT useful for inhibiting expression of HIF-1 and inducing cytotoxicity in  
 PT several cancer cells.

XX Claim 6; SEQ ID NO 4; 35pp; English.  
 XX The invention describes a compound, RX-0047 or RX-0149 targeted to a  
 CC nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),  
 CC where the oligonucleotide compound inhibits the expression of human HIF-  
 CC 1. Also described are: a method of inhibiting the expression of HIF-1 in  
 CC human cells or tissues; and a method of inducing cytotoxicity in a cancer  
 CC cell. Specifically claimed are RX-0047 and RX-0149 compounds having a  
 CC fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5'

CC atagccaccagtgtccaa 3' and SEQ ID NO. 4, 5' ggagctaacatctccaagtc 3',  
 CC respectively). The compounds are useful for inhibiting the expression of  
 CC HIF-1 and inducing the cytotoxicity in several cancer cells. The  
 CC antisense compounds are also useful for preventing or delaying infection,  
 CC inflammation, or tumour formation. This sequence represents a human HIF-1  
 CC antisense oligonucleotide.

XX SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 13; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.7; Indels 0; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 0;

QY 1 GGAGCTAACATCTCCAAGTC 20  
 DB 1 GGAGCTAACATCTCCAAGTC 20

RESULT 3  
 ABZ76611  
 ID ABZ76611 standard; DNA; 49 BP.

XX AC ABZ76611;

XX DT 30-APR-2003 (first entry)

XX DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:24.

XX KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;  
 XX hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;  
 XX tumour; nuclear localisation signal; oxygen dependent degradation domain;  
 XX NLS; ODD; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200299104-A1.

XX PD 12-DEC-2002.

XX PF 04-JUN-2002; 2002WO-JP005482.

XX PR 05-JUN-2001; 2001JP-00169948.

XX PR 05-JUN-2001; 2001JP-00169949.

XX PA (POKK) POLA CHEM IND INC.

XX PA (HIERA) HIRAKA M.

XX PA (KOND/) KONDOSH S.

XX PI Hiraoka M, Kondoh S, Harada H;

XX DR WPI; 2003-148670/14.

XX New DNA encoding a polypeptide imparting relative stability under hypoxic  
 PT conditions to proteins within the cell, useful for treatment of cancer  
 PT and improvement of microbial fermentation.

XX Example; Page 24; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1  
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LQLEMLAPYIPMDDDFQL  
 CC see ABP57669) (I), or encoding a fusion protein containing at least 16  
 CC residues of (I), a nuclear localisation signal (NLS), and another  
 CC protein, and imparting relative stability under specific conditions of  
 CC oxygen concentration within the cell. Also described: (1) vectors  
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing  
 CC the fusion protein by culture of the transformed cells; (4) detecting  
 CC hypoxic conditions in cells by monitoring the stability of the protein  
 CC fused to (I) in cells transformed by vectors containing the DNA; (5)  
 CC regulating the stability of proteins within the cell by transformation  
 CC with the DNA; (6) inhibiting the development of cells under hypoxic  
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the  
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen  
 CC tension. (I) has cytostatic activity, and can be used for the

CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a  
 CC solid tumour, and in gene therapy; (1) can be used in industrial  
 CC microbial fermentation, and in medicine, especially in the treatment of  
 CC tumours containing hypoxic regions. The present sequence represents a PCR  
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)  
 CC domain, which is used in an example from the present invention  
 XX  
 SQ Sequence 49 BP; 15 A; 11 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 3;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20

Db 26 GGAGCTAACATCTCCAAAGTC 45

RESULT 4

AA156916

ID AAL56916 standard; DNA; 16 BP.

XX AAL56916;

DT 11-MAR-2004 (first entry)

XX Human hypoxia-inducible factor-1 alpha antisense oligo #12.

XX HIF-1alpha; hypoxia-inducible factor-1 alpha; human; antisense; cancer;  
 KW pre-eclampsia; cytostatic; gynaecological; antiinflammatory; neurotropic;  
 KW neuroprotective; ss.

XX Homo sapiens.

OS WO2003085110-A2.

PN 16-OCT-2003.

XX 04-APR-2003; 2003WO-IB001758.

XX 05-APR-2002; 2002US-0370126P.

XX (CURE-) CUREON AS.

XX Thru CA, Hog AM, Kristjansen PEG;

XX WPI; 2003-812728/76.

XX New oligonucleotide that modulates hypoxia-inducible factor-1alpha,  
 PT useful for treating e.g. cancer or Alzheimer's disease.

XX Claim 1; Page 41; Opp; English.

XX The present invention relates to compounds capable of modulating hypoxia-  
 CC inducible factor-1alpha (HIF1a). The compounds are used to treat patients  
 CC with, or at risk of developing, cancer (e.g. of breast, prostate,  
 CC pancreas, lung), pre-eclampsia, inflammatory bowel disease or Alzheimer's  
 CC disease, for modulating angiogenesis, proliferation of erythrocytes and  
 CC other cells, iron, glucose and energy metabolism, pH regulation, tissue  
 CC invasion, apoptosis, multiple drug resistance, cellular stress responses,  
 CC and matrix metabolism, especially apoptosis where modulation is  
 CC sensitivity to an apoptotic stimulus, particularly a chemotherapeutic  
 CC agent and for inhibiting proliferation of cells (especially cancer cells)  
 CC in vitro. The present sequence is an antisense oligonucleotide against  
 CC HIF1alpha identified in the exemplification of the invention  
 XX

SQ Sequence 16 BP; 5 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 10; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3; 1e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAAAGT 19

Db 1 GCTAACATCTCCAAAGT 16

RESULT 5

AEAL5801

ID AEAL5801 standard; DNA; 21 BP.

XX AEAL5801;

DT 28-JUL-2005 (first entry)

DE Human Enterobacterium detection-related PCR primer SeqID33.

XX microorganism detection; microorganism identification; DNA detection;  
 KW DNA amplification; enterobacteriaceae infection; antibacterial; PCR;  
 KW primer; ss.

XX Bacteria.

XX JP2005124495-A.

XX 19-MAY-2005.

XX 24-OCT-2003; 2003JP-00364188.

XX 24-OCT-2003; 2003JP-00364188.

XX (HONS ) YAKULT HONSHA KK.

XX WPI; 2005-359465/37.

XX Novel primer comprising specific nucleotide sequences, useful for  
 PT detection and identification of human Enterobacterium such as Clostridium  
 PT butyricum.

XX Claim 1; SEQ ID NO 33; 20pp; Japanese.

XX This invention relates to a novel PCR primer for detecting human  
 CC Enterobacterium, comprising one of 39 fully defined 18-26 nucleotide  
 CC sequences (SEQ ID No. 1-39) given in the specification or a sequence  
 CC complementary to the above mentioned base sequence. The invention enables  
 CC rapid and convenient detection and identification of human  
 CC Enterobacterium. The present sequence is that of a PCR primer which was  
 CC used for detecting human Enterobacterium in the method of the invention.

SQ Sequence 21 BP; 4 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 14; Length 21;

Best Local Similarity 85.0%; Pred. No. 8.2e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20

Db 2 GGAGCTTGCTTCTCCAAAGTC 21

RESULT 6

AEC27934

ID AEC27934 standard; DNA; 26 BP.

XX AEC27934;

DT 17-NOV-2005 (first entry)

DE Human allele-specific oligonucleotide #3954.

XX Haplotype mapping; genetic marker; single nucleotide polymorphism; SNP;  
 KW major histocompatibility complex; MHC; HLA; human leukocyte antigen;  
 KW immune disorder; inflammation; inflammatory bowel disease;  
 KW ulcerative colitis; Crohn's disease; rheumatoid arthritis; diabetes;  
 KW diabetes mellitus; myasthenia gravis; vitiligo; Graves disease;  
 KW Hashimoto's disease; Addison's disease; gastritis; autoimmune hepatitis;

KW rheumatism; systemic lupus erythematosus; scleroderma; polymyositis;  
 KW dermatomyositis; pernicious anemia; primary biliary cirrhosis;  
 KW idiopathic thrombocytopenia purpura; Sjogrens syndrome;  
 KW multiple sclerosis; Reiter's syndrome; psoriasis; antiinflammatory;  
 KW gastrointestinal-gen.; antiulcer; immunomodulator; immunosuppressive;  
 KW antiarthritic; antirheumatic; antidiabetic; muscular-gen.;  
 KW neuroprotective; dermatological; antithyroid; hepatotropic; antianemic;  
 KW SNP detection.  
 KW SNP detection.  
 OS Homo sapiens.  
 XX WO2005082110-A2.  
 XX 09-SEP-2005.  
 XX 28-FEB-2005; 2005WO-US006628.  
 XX 26-FEB-2004; 2004US-0547823P.  
 XX (ILLU-) ILLUMINA INC.  
 XX Oliphant A, Murray S;  
 XX WPI; 2005-638856/65.  
 XX Identifying single nucleotide polymorphism (SNP) haplotype that  
 XX correlates with the HLA type, useful for diagnosing an immunological or  
 XX inflammatory condition, comprises providing SNPs in the major  
 XX histocompatibility complex region.  
 XX Example 1; SEQ ID NO 3954; 175pp; English.  
 XX The invention relates to a method of identifying the nucleotide for each  
 XX of a set of single nucleotide polymorphisms (SNPs) in the major  
 XX histocompatibility complex (MHC) region in a population of individuals,  
 XX comprising providing the HLA type for the individuals and identifying an  
 XX SNP haplotype in the population that correlates with the HLA type, where  
 XX the SNP haplotype comprises the SNPs in the MHC region. The invention  
 XX also relates to a method of predicting the HLA type of an individual, a  
 XX method of determining the presence or absence of an allelic variant of an  
 XX MHC gene in an individual, a method of identifying an SNP haplotype that  
 XX correlates with susceptibility to a disease or condition, and a method of  
 XX determining the susceptibility of an individual to a disease or  
 XX condition. The disease or condition is an immune disorder or inflammatory  
 XX condition selected from inflammatory bowel disease, ulcerative colitis,  
 XX Crohn's disease, rheumatoid arthritis, diabetes, diabetes mellitus,  
 XX myasthenia gravis, vitiligo, Graves disease, Hashimoto's disease,  
 XX Addison's disease, gastritis, autoimmune hepatitis, rheumatism, systemic  
 XX lupus erythematosus, systemic sclerosis, polymyositis, dermatomyositis,  
 XX pernicious anemia, primary biliary cirrhosis, idiopathic thrombocytopenia  
 XX purpura, Sjogren's syndrome, multiple sclerosis, Reiter's syndrome and  
 XX psoriasis. This sequence represents a human allele-specific  
 XX oligonucleotide used in the scope of the invention.  
 XX Sequence 26 BP; 5 A; 7 C; 4 G; 10 T; 0 U; 0 Other;  
 SQ  
 Query Match 71.0%; Score 14.2; DB 14; Length 26;  
 Best Local Similarity 84.2%; Pred. No. 2.7e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GAGCTAACATCTCCAAATC 20  
 DB 5 GACCTAACATCTCCAAATC 23  
 RESULT 7  
 AEC25568  
 ID AEC25568 standard; DNA; 26 BP.  
 XX AEC25568;  
 XX 17-NOV-2005 (first entry)

XX Human allele-specific oligonucleotide #1588.  
 DE Haplotype mapping; Genetic marker; single nucleotide polymorphism; SNP;  
 XX major histocompatibility complex; MHC; HLA; human leukocyte antigen;  
 KW immune disorder; inflammation; inflammatory bowel disease;  
 KW ulcerative colitis; Crohns disease; rheumatoid arthritis; diabetes;  
 KW diabetes mellitus; myasthenia gravis; vitiligo; Graves disease;  
 KW Hashimoto's disease; Addison's disease; gastritis; autoimmune hepatitis;  
 KW rheumatism; systemic lupus erythematosus; scleroderma; polymyositis;  
 KW dermatomyositis; pernicious anemia; primary biliary cirrhosis;  
 KW idiopathic thrombocytopenia purpura; Sjogrens syndrome;  
 KW multiple sclerosis; Reiter's syndrome; psoriasis; antiinflammatory;  
 KW gastrointestinal-gen.; antiulcer; immunomodulator; immunosuppressive;  
 KW antiarthritic; antirheumatic; antidiabetic; muscular-gen.;  
 KW neuroprotective; dermatological; antithyroid; hepatotropic; antianemic;  
 KW hemostatic; ophthalmological; uropathic; antipsoriatic; ss;  
 KW SNP detection.  
 OS Homo sapiens.  
 XX WO2005082110-A2.  
 XX 09-SEP-2005.  
 XX 28-FEB-2005; 2005WO-US006628.  
 XX 26-FEB-2004; 2004US-0547823P.  
 XX (ILLU-) ILLUMINA INC.  
 XX Oliphant A, Murray S;  
 XX WPI; 2005-638856/65.  
 XX Identifying single nucleotide polymorphism (SNP) haplotype that  
 XX correlates with the HLA type, useful for diagnosing an immunological or  
 XX inflammatory condition, comprises providing SNPs in the major  
 XX histocompatibility complex region.  
 XX Example 1; SEQ ID NO 1588; 175pp; English.  
 XX The invention relates to a method of identifying the nucleotide for each  
 XX of a set of single nucleotide polymorphisms (SNPs) in the major  
 XX histocompatibility complex (MHC) region in a population of individuals,  
 XX comprising providing the HLA type for the individuals and identifying an  
 XX SNP haplotype in the population that correlates with the HLA type, where  
 XX the SNP haplotype comprises the SNPs in the MHC region. The invention  
 XX also relates to a method of predicting the HLA type of an individual, a  
 XX method of determining the presence or absence of an allelic variant of an  
 XX MHC gene in an individual, a method of identifying an SNP haplotype that  
 XX correlates with susceptibility to a disease or condition, and a method of  
 XX determining the susceptibility of an individual to a disease or  
 XX condition. The disease or condition is an immune disorder or inflammatory  
 XX condition selected from inflammatory bowel disease, ulcerative colitis,  
 XX Crohn's disease, rheumatoid arthritis, diabetes, diabetes mellitus,  
 XX myasthenia gravis, vitiligo, Graves disease, Hashimoto's disease,  
 KW Addison's disease, gastritis, autoimmune hepatitis, rheumatism, systemic  
 KW lupus erythematosus, systemic sclerosis, polymyositis, dermatomyositis,  
 KW pernicious anemia, primary biliary cirrhosis, idiopathic thrombocytopenia  
 KW purpura, Sjogren's syndrome, multiple sclerosis, Reiter's syndrome and  
 KW psoriasis. This sequence represents a human allele-specific  
 KW oligonucleotide used in the scope of the invention.  
 XX Sequence 26 BP; 6 A; 7 C; 3 G; 10 T; 0 U; 0 Other;  
 SQ  
 Query Match 71.0%; Score 14.2; DB 14; Length 26;  
 Best Local Similarity 84.2%; Pred. No. 2.7e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GAGCTAACATCTCCAAATC 20  
 DB 5 GACCTAACATCTCCAAATC 23

CC oligonucleotide comprises a 5'

CC conditions, using the fusion protein; (7) fusion proteins encoded by the  
CC DNA; and (8) stabilisation of cells under specific conditions of oxygen  
CC tension. (i) has cytostatic activity, and can be used for the  
CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a  
CC solid tumour, and in gene therapy. (i) can be used in industrial  
CC microbial fermentation, and in medicine, especially in the treatment of  
CC tumours containing hypoxic regions. The present sequence represents a PCR  
CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)  
CC domain, which is used in an example from the present invention  
XX  
SQ Sequence 49 BP; 15 A; 10 C; 11 G; 13 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 8; Length 49;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTC 14  
|||  
Db 35 GGAGCTAACATCTC 48

RESULT 10  
AC111456/c  
ID AC111456 standard; DNA; 25 BP.

XX AC111456;  
XX  
XX  
XX 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 11447.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 11447; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific

CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

XX SQ Sequence 25 BP; 7 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 9; Length 25;  
Best Local Similarity 88.2%; Pred. No. 4.4e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAAGTC 20  
|||  
Db 20 GCGACATCTGCAAGTC 4

RESULT 11

AED66358  
ID AED66358 standard; DNA; 36 BP.

XX AED66358;

XX 29-DEC-2005 (first entry)

XX Recombinant cytochrome P450 related P4503A4-Hsp70 sequence N.

XX expression; cytochrome P450; heat shock protein; protein synthesis;  
KW protein folding; gene expression; Hsp70; ds.

XX Unidentified.

XX KR2005028279-A.

XX 22-MAR-2005.

XX 18-SEP-2003; 2003KR-00065447.

XX 18-SEP-2003; 2003KR-00065447.

XX (AHNT/) AHN T H.

XX Ahn TH, Yang SY;

XX WPI; 2005-579519/59.

XX Method for increasing protein expression and catalytic activity of  
PT recombinant cytochrome P450 enzymes by co-expression with genes encoding  
PT heat shock proteins which function as molecular chaperone.

XX Disclosure; Page 3; 8pp; Korean.

XX The invention relates to a method for increasing protein expression and  
CC catalytic activity of recombinant cytochrome P450 enzymes by co-  
CC expression with genes encoding heat shock proteins (HSPs), where the heat  
CC shock proteins function as a molecular chaperone that regulate other  
CC protein synthesis and translocation, protein folding, gene expression,  
CC protein hydrolysis, protein aggregation, etc., so that the heat shock  
CC proteins induce increased protein expression and catalytic activity of  
CC recombinant cytochrome P450 enzymes. The method for increasing protein  
CC expression and catalytic activity of recombinant cytochrome P450 enzymes  
CC comprises co-expression of the recombinant cytochrome P450 enzyme genes  
CC with genes encoding heat shock proteins Hsp70 and HDJ-1, wherein the  
CC recombinant cytochrome P450 enzyme genes and the heat shock protein genes  
CC are isolated from human or rat; the recombinant cytochrome P450 enzyme  
CC genes and the heat shock protein genes are contained in one open reading  
CC frame; and the heat shock proteins induce increased amount and catalytic  
CC activity of the recombinant cytochrome P450 enzymes. This sequence  
CC represents DNA relating to the present invention.

XX Sequence 36 BP; 10 A; 10 C; 13 G; 3 T; 0 U; 0 Other;

```
Query Match          69.0%; Score 13.8; DB 14; Length 36;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAA 17
DB 12 GGAGCTAACATGCGCAA 28

RESULT 12
AED66354
ID AED66354 standard; DNA; 36 BP.
XX
AC AED66354;
XX
DT 29-DEC-2005 (first entry)
XX
DE Recombinant cytochrome P450 related P450IA2-Hsp70 sequence N.
XX
KW expression; cytochrome P450; heat shock protein; protein synthesis;
KW protein folding; gene expression; Hsp70; ds.
XX
OS Unidentified.
XX
FN KR2005028279-A.
XX
PD 22-MAR-2005.
XX
PF 18-SEP-2003; 2003KR-00065447.
XX
PR 18-SEP-2003; 2003KR-00065447.
XX
PA (AHNT/) AHN T H.
XX
PI Ahn TH, Yang SY;
XX
DR WPI; 2005-579519/59.
XX
PT Method for increasing protein expression and catalytic activity of
PT recombinant cytochrome p450 enzymes by co-expression with genes encoding
PT heat shock proteins which function as molecular chaperone.
XX
PS Disclosure; Page 2; 8pp; Korean.
XX
CC The invention relates to a method for increasing protein expression and
CC catalytic activity of recombinant cytochrome P450 enzymes by co-
CC expression with genes encoding heat shock proteins (HSPs), where the heat
CC shock proteins function as a molecular chaperone that regulate other
CC protein synthesis and translocation, protein folding, gene expression,
CC protein hydrolysis, protein aggregation, etc., so that the heat shock
CC proteins induce increased protein expression and catalytic activity of
CC recombinant cytochrome P450 enzymes. The method for increasing protein
CC expression and catalytic activity of recombinant cytochrome P450 enzymes
CC comprises co-expression of the recombinant cytochrome P450 enzyme genes
CC with genes encoding heat shock proteins Hsp70 and HDJ-1, wherein the
CC recombinant cytochrome P450 enzyme genes and the heat shock protein genes
CC are isolated from human or rat; the recombinant cytochrome P450 enzyme
CC genes and the heat shock protein genes are contained in one open reading
CC frame; and the heat shock proteins induce increased amount and catalytic
CC activity of the recombinant cytochrome P450 enzymes. This sequence
CC represents DNA relating to the present invention.
XX
SQ Sequence 36 BP; 11 A; 11 C; 10 G; 4 T; 0 U; 0 Other;

Query Match          69.0%; Score 13.8; DB 14; Length 36;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAA 17
DB 13 GGAGCTAACATGCGCAA 29

RESULT 13
ABZ23749
ID ABZ23749 standard; DNA; 41 BP.
XX
AC ABZ23749;
XX
DT 26-MAR-2003 (first entry)
XX
DE Human membrane vacuole transportation related protein 10.23 probe 1.
XX
KW Human; membrane vacuole transportation protein; 10.23; malignant tumour;
KW haemopathy; human immunodeficiency virus; HIV; immunological disease;
KW inflammation; probe; ss.
XX
OS Homo sapiens.
XX
PN CN1345830-A.
XX
PD 24-APR-2002.
XX
PF 29-SEP-2000; 2000CN-00125514.
XX
PR 29-SEP-2000; 2000CN-00125514.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-584316/63.
XX
PT A novel human membrane vacuole transportation related protein 10.23
PT polypeptide, useful for curing several diseases e.g. malignant tumor,
PT hemopathy, HIV infection, immunological disease and various inflammations
PT and epilepsy.
XX
PS Example 6; Page 19 (disclosure); 33pp; Chinese.
XX
CC The invention relates to a human membrane vacuole transportation related
CC protein 10.23. Also disclosed are the polynucleotide encoding the
CC polypeptide, and a method for preparing the polypeptide using DNA
CC recombination techniques. The polypeptide is useful for curing several
CC diseases including, malignant tumours, haemopathy, human immunodeficiency
CC virus (HIV) infection, immunological disease and various inflammations.
CC The current sequence represents a human membrane vacuole transportation
CC related protein 10.23 related probe sequence
XX
SQ Sequence 41 BP; 9 A; 15 C; 11 G; 6 T; 0 U; 0 Other;

Query Match          69.0%; Score 13.8; DB 6; Length 41;
Best Local Similarity 88.2%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAACTC 20
DB 23 GCTAACAGTCTCCAAGTC 39

RESULT 14
ABZ23750
ID ABZ23750 standard; DNA; 41 BP.
XX
AC ABZ23750;
XX
DT 26-MAR-2003 (first entry)
XX
DE Human membrane vacuole transportation related protein 10.23 probe 2.
XX
KW Human; membrane vacuole transportation protein; 10.23; malignant tumour;
KW haemopathy; human immunodeficiency virus; HIV; immunological disease;
KW inflammation; probe; ss.
XX
OS Homo sapiens.
```

XX CN1345830-A.  
 XX PD 24-APR-2002.  
 XX PP 29-SEP-2000; 2000CN-00125514.  
 XX PR 29-SEP-2000; 2000CN-00125514.  
 XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
 XX PI Mao Y, Xie Y;  
 XX DR WPI; 2002-584316/63.  
 XX A novel human membrane vacuole transportation related protein 10.23  
 PT polypeptide, useful for curing several diseases e.g. malignant tumor,  
 PT hemopathy, HIV infection, immunological disease and various inflammations  
 PT and epilepsy.  
 XX Example 6; Page 19 (disclosure); 33pp; Chinese.  
 XX The invention relates to a human membrane vacuole transportation related  
 CC protein 10.23. Also disclosed are the polynucleotide encoding the  
 CC polypeptide, and a method for preparing the polypeptide using DNA  
 CC recombination techniques. The polypeptide is useful for curing several  
 CC diseases including, malignant tumors, haemopathy, human immunodeficiency  
 CC virus (HIV) infection, immunological disease and various inflammations.  
 CC The current sequence represents a human membrane vacuole transportation  
 CC related protein 10.23 related probe sequence  
 XX  
 XX Sequence 41 BP; 9 A; 15 C; 11 G; 6 T; 0 U; 0 Other;  
 Query Match 69.0%; Score 13.8; DB 6; Length 41;  
 Best Local Similarity 88.2%; Pred. No. 4.7e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 GCTAACATCTCCAAGTC 20  
 Db 23 GGTAAACAGCTCCAAGTC 39  
 RESULT 15  
 ADO31172/c  
 ID ADO31172 standard; DNA; 27 BP.  
 XX  
 AC ADO31172;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Human germinal center associated nuclear protein gene primer #26.  
 XX  
 KW ss; primer; virucide; viral antigen inhibitor; transgenic;  
 KW germinal center associated nuclear protein; GAMP; antibody;  
 KW virus infection; human immunodeficiency virus; hepatitis C virus.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2004040971-A1.  
 XX  
 PD 21-MAY-2004.  
 XX  
 PF 07-NOV-2003; 2003WO-JP014221.  
 XX  
 PR 07-NOV-2002; 2002WO-JP011598.  
 XX  
 PA (IMMU-) IMMUNOKICK INC.  
 XX  
 PI Sakaguchi N;  
 XX  
 DR WPI; 2004-411378/38.  
 XX  
 PT Transgenic mammal transformed with germinal center associated nuclear

PT protein (GAMP) gene for production of high-affinity antibodies as  
 PT diagnostic reagents and disease therapy.  
 XX  
 PS Example 10; SEQ ID NO 30; 214pp; Japanese.  
 XX  
 CC The invention relates to transgenic non-human animals and their offspring  
 CC which are transformed with germinal center associated nuclear protein  
 CC (GAMP) gene. The GAMP gene, encoded protein and transgenic animals  
 CC express GAMP can be used for the production of high-affinity antibodies  
 CC to viral antigens for treatment and prevention of infection by viruses  
 CC such as human immunodeficiency virus and hepatitis C virus. This sequence  
 CC corresponds to a PCR primer to amplify a the human GAMP gene.  
 XX  
 SQ Sequence 27 BP; 6 A; 4 C; 8 G; 9 T; 0 U; 0 Other;  
 Query Match 68.0%; Score 13.6; DB 12; Length 27;  
 Best Local Similarity 80.0%; Pred. No. 5.6e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 GGAGCTAACATCTCCAAGTC 20  
 Db 23 GGTGAACATCTCAAGTC 4  
 Search completed: May 21, 2006, 22:31:22  
 Job time : 390 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:49:17 ; Search time 2196 Seconds  
(without alignments)  
509.284 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggaagtaacattctcaagtc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 194034

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: gb\_est1.\*
- 2: gb\_est3.\*
- 3: gb\_est4.\*
- 4: gb\_est5.\*
- 5: gb\_est6.\*
- 6: gb\_est7.\*
- 7: gb\_est8.\*
- 8: gb\_est9.\*
- 9: gb\_est10.\*
- 10: gb\_est11.\*
- 11: gb\_est12.\*
- 12: gb\_est13.\*
- 13: gb\_est14.\*
- 14: gb\_est15.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	72.0	26	11	AZ352012
2	14.2	71.0	47	11	AZ860255
3	13.8	69.0	49	1	AI348359
4	13.4	67.0	50	4	CA795439
5	13.2	66.0	47	11	AZ362217
6	13.2	66.0	47	14	CT391862
7	13.2	66.0	49	12	CC88587
8	13.2	66.0	50	11	AZ774523
9	12.8	64.0	32	13	CZ918458
10	12.8	64.0	41	11	AZ357818
11	12.6	63.0	28	12	CC795628
12	12.4	62.0	34	1	AI194779
13	12.2	61.0	28	13	CZ917814
14	12.2	61.0	35	11	BZ381186
15	12.2	61.0	37	11	AZ989635
16	12.2	61.0	46	14	AL946937
17	12.2	61.0	48	8	CV191608
18	12	60.0	33	14	AJ529162
19	12	60.0	33	14	ATH529282

c	20	12	60.0	41	14	AG191947
c	21	11.8	59.0	29	1	AM111394
c	22	11.8	59.0	36	11	AZ785517
c	23	11.8	59.0	43	1	AA908443
c	24	11.6	58.0	31	11	AZ473316
c	25	11.6	58.0	32	11	AZ806107
c	26	11.6	58.0	36	1	AU258458
c	27	11.6	58.0	38	11	AZ776209
c	28	11.6	58.0	39	14	BX289673
c	29	11.6	58.0	42	11	BH909732
c	30	11.6	58.0	44	14	AL771809
c	31	11.6	58.0	46	14	BX352523
c	32	11.6	58.0	47	11	AZ321341
c	33	11.6	58.0	48	11	AZ797513
c	34	11.6	58.0	49	11	AZ450961
c	35	11.6	58.0	49	14	BX289417
c	36	11.4	57.0	44	14	DX060578
c	37	11.2	56.0	28	10	R60473
c	38	11.2	56.0	30	12	CC798230
c	39	11.2	56.0	35	11	AZ806105
c	40	11.2	56.0	37	11	AZ592491
c	41	11.2	56.0	37	12	CG715229
c	42	11.2	56.0	37	14	AG199668
c	43	11.2	56.0	40	11	BH405909
c	44	11.2	56.0	40	11	BH904515
c	45	11.2	56.0	45	1	AA276118

#### ALIGNMENTS

RESULT 1	AZ352012	26 bp	DNA	linear	GSS 29-SEP-2000
LOCUS	1M0090M13P	Mouse 10kb plasmid	UUGCLM library	Mus musculus genomic	
DEFINITION	clone UUGCLM0090M13 F, genomic survey sequence.				
ACCESSION	AZ352012				
VERSION	AZ352012.1	GI:10431249			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 26)				
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0090 row: M column: 13 Seq primer: CGTTGTAACGACGCCAGT Class: plasmid ends High quality sequence stop: 26. Location/Qualifiers 1..26 /organism="Mus musculus" /mol_type="genomic DNA" /strain="CS7BL/6J" /db_xref="taxon:10090" /clone="UUGCLM0090M13" /sex="Male"				



/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 72.0%; Score 14.4; DB 11; Length 26;  
 Best Local Similarity 93.8%; Pred. No. 1.5e+04;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAA 17

Db 2 GAGCTCACATCTCCAA 17

## RESULT 2

AZ860255/c

LOCUS

2M0166004F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0166004 F, genomic survey sequence.

AZ860255

VERSION

AZ860255.1 GI:13055225

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 47)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0166 row: J column: 04

Seq primer: CGTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 47.

Location/Qualifiers

1. .47

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0166J04"

## FEATURES

source

1. .47

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0166J04"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

## ORIGIN

Query Match 71.0%; Score 14.2; DB 11; Length 47;  
 Best Local Similarity 84.2%; Pred. No. 2.2e+04;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAAATC 20

Db 47 GAGCAAGCATCTCCAAATC 29

## RESULT 3

A1348359/c

LOCUS

DEFINITION

Q020F09.x1 NCI CGAP Lu5 Homo sapiens CDNA clone IMAGE:1909097 3,

similar to SW:NM\_ HUMAN Q13145 PUTATIVE TRANSMEMBRANE PROTEIN NMA

PRECURSOR. ; mRNA sequence.

ACCESSION

A1348359

VERSION

A1348359.1 GI:4085565

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1 (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgsaps-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 696 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. .49

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1909097"

## FEATURES

source

1. .49

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1909097"

```

/tissue_type="carcinoid"
/lab_host="DH108"
/clone_lib="NCI_CGAP_Lu5"
/notes="Organ: lung; Vector: pT73D-PacI; 1st strand cDNA
was prepared from neuroendocrine lung carcinoid, and was
then primed with a Not I - oligo(dT) primer.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library is
normalized. Library was constructed by Bento Soares and M.
Fatima Bonaldo."

```

## ORIGIN

```

Query Match      69.0%; Score 13.8; DB 1; Length 49;
Best Local Similarity 88.2%; Pred. No. 3.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 GGAGCTAACATCTCCAA 17
    |||||

```

```

DB 38 GTAGCTAACTCTCCAA 22
    |||||

```

## RESULT 4

```

CA795439/c
LOCUS      50 bp mRNA linear EST 05-DEC-2002
DEFINITION Cac_BL_2476 Cac_BL (Bean and Leaf from Amelonardo type Cacao)
Theobroma cacao cDNA clone Cac_BL_2476 5', mRNA sequence.
CA795439
VERSION
KEYWORDS EST.
SOURCE Theobroma cacao (cacao)
ORGANISM Theobroma cacao

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
Theobroma.

```

## REFERENCE

```

1 (bases 1 to 50)
Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
Retzel,E.R. and Jones,C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
Planta 216 (2), 255-264 (2002)
12447539
Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.affem.com
Seq primer: T3.

```

## FEATURES

source

```

1..50
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac BL 2476"
/issue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF"
/clone_lib="Cac_BL (Bean and Leaf from Amelonardo type
Cacao)"
/notes="Vector: pBK-CMV; Bean and leaf tissue from an
Amelonado type Cacao tree."

```

## ORIGIN

```

Query Match      67.0%; Score 13.4; DB 4; Length 50;
Best Local Similarity 93.3%; Pred. No. 5.8e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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QY 2 GAGCTAACATCTCCA 16
    |||||

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DB 43 GAGCTAACACCTCCA 29
    |||||

```

## RESULT 5

AZ362217

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..47

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGGCM10107B16"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGGCM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity

Matches

15; Conservative

0; Mismatches

3; Indels

0; Gaps

0;

QY

3 ACCTAACATCTCCAAGTC 20

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Db      18 AGATAACATTTTCAAGTC 35

RESULT 6
LOCUS   CT391862
DEFINITION
Sus scrofa genomic clone pigE-4888, genomic survey sequence.
ACCESSION
CT391862
VERSION  CT391862.1 GI:79619301
KEYWORDS
GSS.
SOURCE   Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE
1 (bases 1 to 47)
Humphray, S.J., Plumb, R.W. and Durham, J.L.
Direct Submission
Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 4888. 4888 is
part of the PigEBAC BAC Library created by Roslin Institute/RFCGR.
Further details: http://www.sanger.ac.uk/Projects/S\_scrofa/.
FEATURES             source
Location/Qualifiers
1..47
/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"
/clone="pigE-4888"
/tissue_type="Blood cells"
/notes="vector pBeloBAC11
sex male"

ORIGIN
Query Match      66.0%; Score 13.2; DB 14; Length 47;
Best Local Similarity 83.3%; Pred. NO. 7.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGCTACATCTTCAAGTC 20
|||||
Db 10 AGCTGACATGTCACAGTC 27

RESULT 7
LOCUS   CC888587/c
DEFINITION
SALK_152070.41.70.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_152070.41.70.x, genomic
survey sequence.
ACCESSION
CC888587
VERSION  CC888587.1 GI:33365375
KEYWORDS
GSS.
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 49)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of

FEATURES             source
Location/Qualifiers
1..50
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0004L06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

TDNA. This sequence lies within an annotated exon of At3g22540.
Class: TDNA tagged.
FEATURES             source
Location/Qualifiers
1..49
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_152070.41.70.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

ORIGIN
Query Match      66.0%; Score 13.2; DB 12; Length 49;
Best Local Similarity 83.3%; Pred. NO. 7.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTTCCCAAGT 19
|||||
Db 21 GATCTAACACACCACCAAGT 4

RESULT 8
LOCUS   AZ774523
DEFINITION
2M0004L06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0004L06 F, genomic survey sequence.
ACCESSION
AZ774523
VERSION  AZ774523.1 GI:12900062
KEYWORDS
GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 50)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0004 row: L column: 06
Seq primer: CTTGTAAACGACGCCCAAGT
Class: plasmid ends
High quality sequence stop: 50.
FEATURES             source
Location/Qualifiers
1..50
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0004L06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

```

Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 66.0%; Score 13.2; DB 11; Length 50;  
Best Local Similarity 83.3%; Pred. No. 7.4e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGCTAACATCTCCAGTC 20  
|||||  
Db 30 AGCTCAGCTCCAGGTC 47  
|||||

## RESULT 9

CZ918458 32 bp DNA linear GSS 08-AUG-2005  
LOCUS 4021009E02.2EL\_y1 4021 - RescueMu Grid V Zea mays genomic, genomic survey sequence.

ACCESSION CZ918458  
VERSION CZ918458.1 GI:71938010  
KEYWORDS GSS.

## SOURCE

Zea mays

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 32)

## REFERENCE

Walbot, V.  
Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)

## JOURNAL

Contact: Walbot V

## COMMENT

Department of Biological Sciences

Stanford University

955 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4021009 row: E column: 02

Class: transposon-tagged.

## FEATURES

Location/Qualifiers

1..32

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A186/B73/K55"

/db\_xref="taxon:4577"

/issue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="4021 - RescueMu Grid V"

/notes="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site 1: BamHI, Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site 'http://www.mutransposon.org/project/RescueMu/'. Grid

V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

Query Match 64.0%; Score 12.8; DB 13; Length 32;  
Best Local Similarity 87.5%; Pred. No. 1.1e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAA 17  
|||||  
Db 8 GAGCAAGCATCTCCAA 23  
|||||

## RESULT 10

AZ357818/c

LOCUS

DEFINITION

1M0099107R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0099107 R, genomic survey sequence.

ACCESSION AZ357818

VERSION AZ357818.1 GI:10471518

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 41)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0099 row: I column: 07

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 41.

Location/Qualifiers

1..41

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0099107"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

```

Query Match      64.0%; Score 12.8; DB 11; Length 41;
Best Local Similarity 87.5%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGAGCTAACATCTCCA 16
    |||||
Db 24 GGGGCTTACATCTCCA 9

```

RESULT 11

LOCUS	CC795628	28 bp	DNA	linear	GSS 01-JUL-2003
DEFINITION	SALK_087613.35.10.x <i>Arabidopsis thaliana</i> TDNA insertion lines <i>Arabidopsis thaliana</i> genomic clone SALK_087613.35.10.x, genomic survey sequence.				

ACCESSION	CC795628
VERSION	CC795628.1
	GI:32390851

**KEYWORDS**  
GSS.

**SOURCE**

ORGANISM  
*Arabidopsis thaliana*  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

## REFERENCE

**AUTHORS** Alonso, J.M., Leisze, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.

**TITLE** A Sequence-Indexed Library of Insertion Mutations in the

Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (STGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left  
TDNA.

**TDNA.**

```

FEATURES
  source
    Class: TDNA tagged.
      Location/Qualifiers
        1..128
          /organism="Arabidopsis thaliana"
          /mol_type="genomic DNA"
          /ecotype="Col-0"
          /db_xref="taxon:1702"

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`/clones="SALK_087613_35_10_x"
 /clone.lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used
 can be found at http://signal.salk.edu/TDNA\_protocols.htm`

## ORIGIN

Query Match	63.0%	Score 12.6;	DB 12;
Best Local Similarity	78.9%	Pred. No. 1.3e+05;	Length 28;
Matches 15;	Conservative	0;	Mismatches 4;
			Indels 0;
			Gaps 0;

QY 1 GGAGCTAACATCTCCAAGT 19

21 GAATCTAAGATCACCAAGT 3

## RESULT 12

AI194779/c  
LOCUS  
DEFINITION

**ACCESSION**

VERSION  
KEYWORDS  
SOURCE  
ORGANISM

## REFERENCE

## AUTHORS

**TITLE**

**JOURNAL  
COMMENT**

## FEATURES

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1.      "name": "Mus musculus",
   /organism="Mus musculus"
   /mol_type="mRNA"
   /strain="C57BL"
   /db_xref="taxon:10090"
   /clone IMAGE:1886446"
   /sex="female"
   /dev stages="adult"
   /lab_host="DH1OB"
   /clone_lib"Sugano mouse
   /note="Organ: liver; Vec
   (CACTGTGG); Site 2: DraI
   was primed with an oligo
   [ATGCGCGTTCCTTTTCTTTTTT
   ligated to a Drail adapter
   and cloned into distinct
   vector (5' site CACTGTGTG
   be used to isolate the cDNA
   performed to exclude fra
   constructed by Dr. Sumio
   Institute of Medical Sci
   sequencing: 5' end primer
   sequence: CAGCTGCACCTGCAGC

```

## ORIGIN

Query Match	62.0%	Score 12.4;	DB 1;	Length 34;
Best Local Similarity	92.9%;	Pred. No. 1.8e+05;		
Matches 13;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0;

3 AGCTAACATCTCCA 16  
Ov

Db 29 AGCTAACATCTTCA 16

RESULT 13

CZ917814

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LOCUS      C2917814          28 bp      DNA          linear      GSS 08-AUG-2005
DEFINITION 4021007A12.2BL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic
survey sequence.
ACCESSION  C2917814
VERSION     C2917814.1  GI:71936909
KEYWORDS    GSS.
SOURCE      Zea mays
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 28)
TITLE      Walbot, V.
JOURNAL     Maize genomic sequences found using engineered RescueMu transposon
COMMENT     Unpublished (2001)
            Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Possible ligation site of ends cut by 2 different endonucleases.
            Reversease complemented post-ligation sequence from source sequence.
            Plate: 4021007 row: A column: 12
            Class: transposon-tagged.
            Location/Qualifiers
                1..28
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /cultivar="mixed background W23/Al88/B73/K55"
                /db_xref="taxon:4577"
                /dev_stage="adult"
                /tissue_type="leaf"
                /lab_hosts="DH10B"
                /clone_lib="4021 - RescueMu Grid V"
                /notes="Organ: leaf; Vector: RescueMu (engineered from
                pBluescript backbone); Site 1: BamHI; Site 2: BglII;
                RescueMu is a 4.9 kb, modified maize Mu transposon
                designed to allow plasmid rescue from total genomic DNA.
                Mu elements insert preferentially into transcription
                units. For more information on RescueMu, go to the web
                site 'http://www.mutransposon.org/project/RescueMu/'. Grid
                V was grown at University of Arizona in 2003. DNA was
                extracted from leaf strips, double digested using BamHI
                and BglII, and ligated to form circular plasmids. DH10B
                cells were transformed and then screened on LB plates with
                ampicillin."

ORIGIN
Query Match      61.0%; Score 12.2; DB 13; Length 28;
Best Local Similarity 82.4%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2  GAGCTAACATCTCCAAG 18
    |||
Db   2  GAAGTCACATCTCCAAG 18

RESULT 14
BZ381186/c      35 bp      DNA          linear      GSS 26-NOV-2002
LOCUS          SALK_116379.23.70.x Arabidopsis thaliana TDNA insertion lines
DEFINITION  Arabidopsis thaliana genomic clone SALK_116379.23.70.x, genomic
survey sequence.
ACCESSION  BZ381186
VERSION     BZ381186.1  GI:25474862
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
ORIGIN
Query Match      61.0%; Score 12.2; DB 11; Length 35;
Best Local Similarity 82.4%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1  GGAGCTAACATCTCCAA 17
    |||
Db   1  GGTGCTAATAGCTCCAA 1

RESULT 15
AZ989635
LOCUS          2M0273K06F Mouse 10kb plasmid TUGC2M library Mus musculus genomic
DEFINITION  clone UUGC2M0273K06 F, genomic survey sequence.
ACCESSION  AZ989635
VERSION     AZ989635.1  GI:13860862
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

```

1  (bases 1 to 35)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
            Location/Qualifiers
                1..35
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /ecotype="Col-0"
                /db_xref="taxon:3702"
                /clone_lib="SALK_116379.23.70.x"
                /notes="Arabidopsis thaliana TDNA insertion lines"
                /notes="PCR was performed on Arabidopsis thaliana lines
                each of which contains one or more TDNA insertion
                elements. The resultant fragment for each line was
                directly sequenced to determine the genomic sequence at
                the site of insertion. Details of the protocols used can
                be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      61.0%; Score 12.2; DB 11; Length 35;
Best Local Similarity 82.4%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1  GGAGCTAACATCTCCAA 17
    |||
Db   1  GGTGCTAATAGCTCCAA 1

RESULT 15
AZ989635      37 bp      DNA          linear      GSS 27-APR-2001
LOCUS          2M0273K06F Mouse 10kb plasmid TUGC2M library Mus musculus genomic
DEFINITION  clone UUGC2M0273K06 F, genomic survey sequence.
ACCESSION  AZ989635
VERSION     AZ989635.1  GI:13860862
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0273 row: K column: 06

```

Seq primer: CGTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 37.

FEATURES

source

1..37  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0273K06"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 61.0%; Score 12.2; DB 11; Length 37;  
Best Local Similarity 82.4%; Pred. No. 2.3e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 4 GCTAACATCTCCCAAGTC 20  
|||||  
Db 2 GCTAACATCTCCCGCC 18

Search completed: May 21, 2006, 23:02:41  
Job time : 2201 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 22:08:44 ; Search time 115.5 Seconds  
(without alignments)  
324.002 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggagctacatctccaagtc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1429044

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /EMC\_Celerra\_SID33/ptodata/2/ina/1\_COMB.seq.\*
- 2: /EMC\_Celerra\_SID33/ptodata/2/ina/5\_COMB.seq.\*
- 3: /EMC\_Celerra\_SID33/ptodata/2/ina/6A\_COMB.seq.\*
- 4: /EMC\_Celerra\_SID33/ptodata/2/ina/6B\_COMB.seq.\*
- 5: /EMC\_Celerra\_SID33/ptodata/2/ina/7\_COMB.seq.\*
- 6: /EMC\_Celerra\_SID33/ptodata/2/ina/H\_COMB.seq.\*
- 7: /EMC\_Celerra\_SID33/ptodata/2/ina/PCTRUS\_COMB.seq.\*
- 8: /EMC\_Celerra\_SID33/ptodata/2/ina/PP\_COMB.seq.\*
- 9: /EMC\_Celerra\_SID33/ptodata/2/ina/RE\_COMB.seq.\*
- 10: /EMC\_Celerra\_SID33/ptodata/2/ina/backfileseq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	13.8	69.0	25	3	US-09-396-196G-88907	Sequence 88907, A
2	13.8	69.0	25	3	US-09-396-196G-88908	Sequence 88908, A
3	13.6	68.0	30	5	US-09-501-328-19	Sequence 19, Appl
4	13.6	68.0	40	3	US-09-014-416-19	Sequence 19, Appl
5	13.6	68.0	41	3	US-09-014-416-50	Sequence 50, Appl
6	13.6	68.0	42	3	US-09-014-416-51	Sequence 51, Appl
7	13.4	67.0	20	3	US-09-198-452A-3110	Sequence 3110, Ap
8	13.4	67.0	25	3	US-09-396-196G-87226	Sequence 87226, A
9	13	65.0	25	3	US-09-396-196G-88906	Sequence 88906, A
10	12.8	64.0	24	3	US-10-002-974-76	Sequence 76, Appl
11	12.8	64.0	24	3	US-10-002-974-77	Sequence 77, Appl
12	12.8	64.0	29	3	US-09-214-718-13	Sequence 13, Appl
13	12.8	64.0	47	3	US-09-422-978-1943	Sequence 1943, Ap
14	12.8	64.0	50	3	US-10-131-827-4910	Sequence 4910, Ap
15	12.8	64.0	50	5	US-10-131-831-4910	Sequence 4910, Ap
16	12.6	63.0	20	3	US-09-657-472-2547	Sequence 2547, Ap
17	12.6	63.0	25	3	US-09-396-196G-25961	Sequence 25961, A
18	12.6	63.0	25	3	US-09-396-196G-74047	Sequence 74047, A
19	12.6	63.0	26	3	US-09-014-416-18	Sequence 18, Appl
20	12.6	63.0	30	4	US-10-206-406A-20	Sequence 20, Appl
21	12.6	63.0	30	3	US-09-474-432B-1384	Sequence 1384, Ap
22	12.6	63.0	38	3	US-09-476-087-1383	Sequence 1383, Ap
23	12.6	63.0	39	2	US-08-537-002A-15	Sequence 15, Appl

c 24	12.6	63.0	39	3	US-08-863-010-15	Sequence 15, Appl
c 25	12.6	63.0	39	3	US-09-024-429-15	Sequence 15, Appl
c 26	12.6	63.0	39	10	5256648-8	Patent No. 5256648
c 27	12.4	62.0	20	2	US-08-117-952-674	Sequence 674, App
c 28	12.4	62.0	25	3	US-09-396-196G-13583	Sequence 13583, A
c 29	12.4	62.0	25	3	US-09-396-196G-34775	Sequence 34775, A
c 30	12.4	62.0	25	3	US-09-396-196G-34776	Sequence 34776, A
c 31	12.4	62.0	25	3	US-09-396-196G-34919	Sequence 34919, A
c 32	12.4	62.0	25	3	US-09-396-196G-34920	Sequence 34920, A
c 33	12.4	62.0	25	3	US-09-396-196G-34931	Sequence 34931, A
c 34	12.4	62.0	25	3	US-09-396-196G-34932	Sequence 34932, A
c 35	12.4	62.0	25	3	US-09-396-196G-34933	Sequence 34933, A
c 36	12.4	62.0	25	3	US-09-396-196G-34934	Sequence 34934, A
c 37	12.4	62.0	25	3	US-09-396-196G-115104	Sequence 115104, A
c 38	12.4	62.0	27	3	US-09-579-420B-7	Sequence 7, Appli
c 39	12.4	62.0	27	3	US-09-579-420B-9	Sequence 9, Appli
c 40	12.4	62.0	27	3	US-09-579-420B-11	Sequence 11, Appl
c 41	12.4	62.0	27	3	US-09-579-420B-13	Sequence 13, Appl
c 42	12.4	62.0	27	3	US-09-579-420B-14	Sequence 14, Appl
c 43	12.4	62.0	27	3	US-10-101-816-10	Sequence 10, Appl
c 44	12.4	62.0	27	3	US-10-101-816-11	Sequence 11, Appl
c 45	12.4	62.0	30	3	US-09-421-365-4	Sequence 4, Appli

#### ALIGNMENTS

RESULT 1  
; Sequence 88907, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396.196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 88907  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-88907

Query Match 69.0%; Score 13.8; DB 3; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCTAACATCTCCCAAGTC 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 7 GCTAACATCTCCATTC 23

RESULT 2  
US-09-396-196G-88908  
; Sequence 88908, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396.196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678



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/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 89908
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-09-396-196G-88908

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Query Match 69.0%; Score 13.8; DB 3; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels

QY 4 GCTAACATCTCCAAGTC 20  
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Db 1 GCTAACATCTCCATTTC 17

RESULT 3  
US-09-501-328-19  
; Sequence 19, Application US/09501328  
; Patent No. 7022320

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/ GENERAL INFORMATION:
/ APPLICANT: Macklin, Michael D.
/ APPLICANT: Fuller, Deborah L.
/ TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS IMMUNIZATION
/ FILE REFERENCE: 7011-0032
/ CURRENT APPLICATION NUMBER: US/09/501,328
/ CURRENT FILING DATE: 2000-02-09
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 30

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description
; OTHER INFORMATION: primer
US-09-501-328-19

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Query Match 68.0%; Score 13.6; DB 5; Length 30;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels

QY 1 GGAGCTAACATCTCCAAGTC 20  
|||||  
Db 1 GGAGCTAGCATGGCCAAGAC 20

RESULT 4  
US-09-014-416-19/c  
; Sequence 19, Application US/09014416  
; Patent No. 6153421

```

/ GENERAL INFORMATION:
/ APPLICANT: Yanagi, Masayuki
/ APPLICANT: Bukh, Jens
/ APPLICANT: Emerson, Susanne U.
/ APPLICANT: Purcell, Robert H.
/ TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
/ TITLE OF INVENTION: US$ THEREOF
/ FILE REFERENCE: 20264276
/ CURRENT APPLICATION NUMBER: US/09/014,416
/ CURRENT FILING DATE: 1998-01-27
/ EARLIER APPLICATION NUMBER: US 60/053,062
/ EARLIER FILING DATE: 1997-07-18
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 19
/ LENGTH: 40
/ TYPE: DNA
/ ORGANISM: Hepatitis C virus
US-09-014-416-19

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Query Match	68.0%;	Score 13.6;	DB 3;	Length 40;
Best Local Similarity	80.0%;	Pred. NO. 1.5e+03;		
Matches 16;	Conservative	0;	Mismatches 4;	Indels

Qy 1 GGAGCTAACATCTCCAAGTC 20  
|||  
Db 33 GGAGCTAACCACTCCAGGCC 14

RESULT 5  
US-09-014-416-50  
; Sequence 50, Application US/09014416  
; Patent No. 6153421

; GENERAL INFORMATION:  
; APPLICANT: Yanagi, Masayuki  
; APPLICANT: Bukh, Jens  
; APPLICANT: Emerson, Susanne U.

```

/ APPLICANT: PURCELL, ROBERT H.
/ TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
/ TITLE OF INVENTION: USES THEREOF
/ FILE REFERENCE: 20264276
/ CURRENT APPLICATION NUMBER: US/09/014,416
/ CURRENT FILING DATE: 1998-01-27
/ EARLIER APPLICATION NUMBER: US 60/053,062
/ EARLIER FILING DATE: 1997-07-18
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 50
/ LENGTH: 41
/ TYPE: DNA
/ ORGANISM: Hepatitis C virus
US-09-014-416-50

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Query Match      68.0%; Score 13.6; DB 3; Length 41;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY  
1 GGAGCTAACATCTCCAAGTC 20  
|||||  
8 GGAGCTAACCACTCCAGGCC 27

RESULT 6  
US-09-014-416-51  
; Sequence 51, Application US/09014416  
; Patent No. 6153421

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: GENERAL INFORMATION:
: APPLICANT: Yanagi, Masayuki
: APPLICANT: Eukh, Jens
: APPLICANT: Emerson, Susanne U.
: APPLICANT: Purcell, Robert H.
: TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: 20264276
: CURRENT APPLICATION NUMBER: US/09/014.416
: CURRENT FILING DATE: 1998-01-27
: EARLIER APPLICATION NUMBER: US 60/053.062
: EARLIER FILING DATE: 1997-07-18
: NUMBER OF SEQ ID NOS: 65
: SOFTWARE: Patentin ver. 2.1
: SEQ ID NO 51
: LENGTH: 42
: TYPE: DNA
: ORGANISM: Hepatitis C virus
: US-09-014-416-51

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Query Match      68.0%; Score 13.6; DB 3; Length 42;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 GGAGCTAACATCTCCAAGTC 20  
|||  
Db 8 GGAGCTAACCACTCCAGGCC 27

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; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88906
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-88906

Query Match      65.0%; Score 13; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GCTAACATCTCCAA 16
        |||||
DB      13 GCTAACATCTCCA 25

RESULT 7
US-09-198-452A-3110
; Sequence 3110, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3110
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-3110

Query Match      67.0%; Score 13.4; DB 3; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCTAACATCTCCAAG 18
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DB      6 GCTGACATCTCCAAG 20

RESULT 8
US-09-396-196G-87226/c
; Sequence 87226, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87226
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-87226

Query Match      67.0%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GAGCTAACATCTCCA 16
        |||||
DB      22 GAGCTAAGATCTCCA 8

RESULT 9
US-09-396-196G-88906
; Sequence 88906, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
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; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88906
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-88906

Query Match      65.0%; Score 13; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GCTAACATCTCCA 16
        |||||
DB      13 GCTAACATCTCCA 25

RESULT 10
US-10-002-974-76/c
; Sequence 76, Application US/10002974
; Patent No. 6858391
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogur, Yasunori
; APPLICANT: Cho, Judy
; APPLICANT: Nicolae, Dan L
; APPLICANT: Bonen, Denise
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06646
; CURRENT APPLICATION NUMBER: US/10/002,974
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-002-974-76

Query Match      64.0%; Score 12.8; DB 3; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GAGCTAACATCTCCAA 17
        |||||
DB      16 GAGCTAACTCTGCAA 1

RESULT 11
US-10-002-974-77/c
; Sequence 77, Application US/10002974
; Patent No. 6858391
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogur, Yasunori
; APPLICANT: Cho, Judy
; APPLICANT: Nicolae, Dan L
; APPLICANT: Bonen, Denise
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06646
; CURRENT APPLICATION NUMBER: US/10/002,974
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 24
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-10-002-974-77

Query Match          64.0%; Score 12.8; DB 3; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAA 17
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Db 16 GAGCTAACTTCTGCAA 1

RESULT 12
US-09-214-718-13
; Sequence 13, Application US/09214718
; Patent No. 6756357
; GENERAL INFORMATION:
; APPLICANT: Laufer, Ralph
; APPLICANT: Di Marco, Annalise
; TITLE OF INVENTION: VARIANTS OF HUMAN CILIARY NEUROTROPHIC
; TITLE OF INVENTION: FACTOR (hcnf) WITH A RANGE OF ACTION DIFFERENT FROM THAT OF
; TITLE OF INVENTION: THE WILD-TYPE MOLECULE
; FILE REFERENCE: ITR0009P
; CURRENT APPLICATION NUMBER: US/09/214,718
; CURRENT FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: PCT/IT97/00163
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: RM96A000492
; PRIOR FILING DATE: 1996-07-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-214-718-13

Query Match          64.0%; Score 12.8; DB 3; Length 29;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAA 17
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Db 13 GAGCCACCATCTCCAA 28

RESULT 13
US-09-422-978-1943/c
; Sequence 1943, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1943
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
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; LOCATION: 24
; OTHER INFORMATION: 99-7493-249 : polymorphic base G or C
US-09-422-978-1943

Query Match          64.0%; Score 12.8; DB 3; Length 47;
Best Local Similarity 87.5%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAAGT 19
   ||||| ||||| |||||
Db 19 GGTCAATCTCCAAGT 4

RESULT 14
US-10-131-827-4910/c
; Sequence 4910, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: LV, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUN
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4910
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4910

Query Match          64.0%; Score 12.8; DB 3; Length 50;
Best Local Similarity 87.5%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAA 17
   ||||| ||||| |||||
Db 32 GAGCTAATATCTCAA 17

RESULT 15
US-10-131-831-4910/c
; Sequence 4910, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: LV, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4910
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-4910
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Query Match 64.0%; Score 12.8; DB 5; Length 50;  
 Best Local Similarity 87.5%; Pred. No. 3.9e+03;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAA 17  
 |||||  
 Db 32 GAGCTAATATCTCATA 17

Search completed: May 21, 2006, 23:25:17  
 Job time : 116.5 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 22:09:18 ; Search time 654 Seconds  
(without alignments)  
375.769 Million cell updates/sec

Title: US-10-766-185-4  
Perfect score: 20  
Sequence: 1 ggagctaacatctccaagtc 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24111450

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
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- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 3	16	80.0	16	8	US-10-407-807-13
C 4	15.8	79.0	25	8	US-10-719-956-576763
C 5	15.8	79.0	25	9	US-10-719-900-163104
C 6	15.4	77.0	25	9	US-10-719-900-213846
C 7	15.4	77.0	25	11	US-10-932-182A-23140
C 8	15.2	76.0	25	11	US-10-932-182A-107428
C 9	15.2	76.0	25	13	US-11-036-317-197855
C 10	15.2	76.0	25	13	US-11-036-317-229502
C 11	15.2	76.0	25	13	US-11-036-317-292030
C 12	15.2	76.0	25	13	US-11-036-317-321919
C 13	15.2	76.0	25	15	US-11-121-849-110453
C 14	15	75.0	50	16	US-11-175-859-56177
C 15	14.8	74.0	19	14	US-11-083-784-429065
C 16	14.8	74.0	19	14	US-11-083-784-1271642
C 17	14.8	74.0	19	15	US-11-101-244-429065

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Sequence 343202,  
Sequence 372970,  
Sequence 556264,  
Sequence 135850,  
Sequence 472809,  
Sequence 789532,  
Sequence 362173,  
Sequence 163892,  
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Sequence 39265, A  
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Sequence 164931,  
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Sequence 787730,  
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Sequence 13104, A  
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Sequence 256488,  
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Sequence 256488,  
Sequence 256505,

18 14.8 74.0 19 15 US-11-101-244-1271642  
19 14.8 74.0 25 8 US-10-719-956-343202  
20 14.8 74.0 25 8 US-10-719-956-372970  
21 14.8 74.0 25 8 US-10-719-956-556264  
22 14.8 74.0 25 9 US-10-719-900-135850  
23 14.8 74.0 25 9 US-10-719-900-472809  
24 14.8 74.0 25 9 US-10-719-900-789532  
25 14.8 74.0 25 15 US-11-121-849-362173  
26 14.8 74.0 25 15 US-11-121-849-665524  
27 14.8 74.0 25 15 US-11-121-849-665525  
28 14.4 72.0 19 14 US-11-083-784-163892  
29 14.4 72.0 19 14 US-11-083-784-1271671  
30 14.4 72.0 19 15 US-11-101-244-163892  
31 14.4 72.0 19 15 US-11-101-244-1271671  
32 14.4 72.0 25 8 US-10-719-956-39265  
33 14.4 72.0 25 9 US-10-719-900-465139  
34 14.4 72.0 25 10 US-10-956-157-164931  
35 14.4 72.0 25 13 US-11-036-317-684060  
36 14.4 72.0 25 13 US-11-036-317-787730  
37 14.4 72.0 25 15 US-11-121-849-98792  
38 14.4 72.0 25 15 US-11-121-849-386481  
39 14.4 72.0 50 16 US-11-175-859-13104  
40 14.2 71.0 19 14 US-11-083-784-240931  
41 14.2 71.0 19 14 US-11-083-784-256488  
42 14.2 71.0 19 14 US-11-083-784-256505  
43 14.2 71.0 19 15 US-11-101-244-240931  
44 14.2 71.0 19 15 US-11-101-244-256488  
45 14.2 71.0 19 15 US-11-101-244-256505

## ALIGNMENTS

## RESULT 1

US-10-766-185-3/c  
; Sequence 3, Application US/10766185  
; Publication No. US20040152655A1  
; GENERAL INFORMATION:  
; APPLICANT: Yoon, Heejeong  
; APPLICANT: Ahn, Chang Ho  
; APPLICANT: Lee, Young Bok  
; APPLICANT: Mao, Lingjun  
; APPLICANT: Jiang, Xiaoming  
; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1  
; FILE REFERENCE: REX 7034  
; CURRENT APPLICATION NUMBER: US/10/766,185  
; CURRENT FILING DATE: 2004-01-28  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: human  
US-10-766-185-3

Query Match 100.0% Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.4; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20  
DB 20 GGAGCTAACATCTCCAAGTC 1

## RESULT 2

US-10-766-185-4  
; Sequence 4, Application US/10766185  
; Publication No. US20040152655A1  
; GENERAL INFORMATION:  
; APPLICANT: Yoon, Heejeong  
; APPLICANT: Ahn, Chang Ho  
; APPLICANT: Lee, Young Bok  
; APPLICANT: Mao, Lingjun

APPLICANT: Jiang, Xiaoming  
TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1  
FILE REFERENCE: REX 7034  
CURRENT APPLICATION NUMBER: US/10/766,185  
CURRENT FILING DATE: 2004-01-28  
NUMBER OF SEQ ID NOS: 130  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 20  
TYPE: DNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: antisense oligonucleotide  
US-10-766-185-4

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.4; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0

QY 1 GGAGCTAACATCTCCAAGTC 20  
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DB 1 GGAGCTAACATCTCCAAGTC 20

RESULT 3  
US-10-407-807-13  
Sequence 13, Application US/10407807  
Publication No. US20040096848A1  
GENERAL INFORMATION:  
APPLICANT: THRUB, CHARLOTTE ALBAEK  
APPLICANT: HOG, ANJA MOLHART  
TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION HIF-1ALPHA  
FILE REFERENCE: 57390 (45120)  
CURRENT APPLICATION NUMBER: US/10/407,807  
CURRENT FILING DATE: 2003-10-23  
PRIOR APPLICATION NUMBER: 60/370,126  
PRIOR FILING DATE: 2002-04-05  
NUMBER OF SEQ ID NOS: 124  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 13  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: oligonucleotide  
US-10-407-807-13

Query Match 80.0%; Score 16; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 16; Conservative 0

QY 4 GCTAACATCTCCAAGT 19  
|||||  
DB 1 GCTAACATCTCCAAGT 16

RESULT 4  
US-10-719-956-576763/c  
Sequence 576763, Application US/10719956  
Publication No. US20040146910A1  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
FILE REFERENCE: 3527.1  
CURRENT APPLICATION NUMBER: US/10/719,956  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,836  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 699466  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 576763  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-10-719-956-576763

Query Match 79.0%; Score 15.8; DB 8; Length 25;  
Best Local Similarity 89.5%; Pred. No. 6.9e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAAGTC 20  
|||||  
DB 22 GAGCGAACATTTCCAAGTC 4

RESULT 5  
US-10-719-900-163104/c  
Sequence 163104, Application US/10719900  
Publication No. US20050026164A1  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528.1  
CURRENT APPLICATION NUMBER: US/10/719,900  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,808  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 163104  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-163104

Query Match 79.0%; Score 15.8; DB 9; Length 25;  
Best Local Similarity 89.5%; Pred. No. 6.9e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGT 19  
|||||  
DB 24 GGAGCGAACATCTCGAAGT 6

RESULT 6  
US-10-719-900-213846/c  
Sequence 213846, Application US/10719900  
Publication No. US20050026164A1  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528.1  
CURRENT APPLICATION NUMBER: US/10/719,900  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,808  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 213846  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-213846

Query Match 77.0%; Score 15.4; DB 9; Length 25;  
Best Local Similarity 94.1%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAAGTC 20  
|||||  
DB 24 GCTAACATCTCCAAGTC 8

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RESULT 7
US-10-932-182A-23140
; Sequence 23140, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23140
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-23140

Query Match          77.0%; Score 15.4; DB 11; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCCAAGTC 20
   ||||| ||||| |||||
DB 5 GCTAGATCTCCCAAGTC 21

RESULT 8
US-10-932-182A-107428
; Sequence 107428, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 107428
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-107428

Query Match          76.0%; Score 15.2; DB 11; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
   ||||| ||||| |||||
DB 5 GGTGCTAAGATCACCACAGTC 24

RESULT 9
US-11-036-317-197855/c
; Sequence 197855, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 292030
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-197855/c

Query Match          76.0%; Score 15.2; DB 13; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
   ||||| ||||| |||||
DB 23 GGAGATGACATGTCCCAAGTC 4

RESULT 11
US-11-036-317-292030/c
; Sequence 292030, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 292030
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-292030/c

Query Match          76.0%; Score 15.2; DB 13; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
   ||||| ||||| |||||
DB 23 GGAGATGACATGTCCCAAGTC 4

RESULT 10
US-11-036-317-229502/c
; Sequence 229502, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 229502
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-229502/c

Query Match          76.0%; Score 15.2; DB 13; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
   ||||| ||||| |||||
DB 22 GGAGATGACATGTCCCAAGTC 3

RESULT 10
US-11-036-317-229502/c
; Sequence 229502, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 229502
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-229502/c

Query Match          76.0%; Score 15.2; DB 13; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
   ||||| ||||| |||||
DB 23 GGAGATGACATGTCCCAAGTC 4

RESULT 11
US-11-036-317-292030/c
; Sequence 292030, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 292030
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-292030/c

Query Match          76.0%; Score 15.2; DB 13; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 GGAGCTAACATCTCCCAAGTC 20
    |||||
Db 20 GGAGATGACATGTCCCAAGTC 1

RESULT 12
US-11-036-317-321919/c
; Sequence 321919, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 321919
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-321919

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 13; Length 25;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
    |||||
Db 21 GGAGATGACATGTCCCAAGTC 2

RESULT 13
US-11-121-849-110453
; Sequence 110453, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 110453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-110453

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 15; Length 25;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
    |||||
Db 1 GGAGTACCATCTGCANATC 20

RESULT 14
US-11-175-859-56177/c
; Sequence 56177, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
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; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56177
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-56177

Query Match
Best Local Similarity 75.0%; Score 15; DB 16; Length 50;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCCAAGTC 20
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Db 32 GCTAACRTCTCTCAAGTC 16

RESULT 15
US-11-083-784-429065
; Sequence 429065, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmavon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 429065
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-429065

Query Match
Best Local Similarity 74.0%; Score 14.8; DB 14; Length 19;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCCAAGT 19
    |||||
Db 1 GAGCUUACUCCUCCAGU 18

Search completed: May 21, 2006, 22:32:00
Job time : 655 secs
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 22:18:38 ; Search time 32.5 Seconds  
(without alignments)  
43.419 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggagctaacatctccaagtc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 387544

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries.

Database : Published Applications NA New.\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.4	77.0	25	7	US-11-217-529-23140 Sequence 23140, A
2	15.2	76.0	25	7	US-11-217-529-107428 Sequence 107428, A
3	14	70.0	25	7	US-11-217-529-35122 Sequence 35122, A
4	13.8	69.0	25	7	US-11-217-529-70037 Sequence 70037, A
5	13.8	69.0	25	7	US-11-217-529-85327 Sequence 85327, A
6	13.6	68.0	25	7	US-11-217-529-46511 Sequence 46511, A
7	13.2	66.0	25	7	US-11-217-529-134913 Sequence 134913, A
8	12.8	64.0	25	7	US-11-217-529-8091 Sequence 8091, Ap
9	12.8	64.0	25	7	US-11-217-529-131839 Sequence 131839, Ap
10	12.8	64.0	50	6	US-10-511-937-2714 Sequence 2714, Ap
11	12.6	63.0	25	7	US-11-217-529-46927 Sequence 46927, A
12	12.6	63.0	25	7	US-11-217-529-84789 Sequence 84789, A
13	12.6	63.0	25	7	US-11-217-529-129113 Sequence 129113, A
14	12.6	63.0	25	7	US-11-217-529-141646 Sequence 141646, A
15	12.6	63.0	25	7	US-11-217-529-170895 Sequence 170895, A
16	12.6	63.0	27	1	US-09-756-0978-97 Sequence 97, Appl
17	12.6	63.0	30	1	US-09-756-0978-94 Sequence 94, Appl
18	12.4	62.0	25	7	US-11-217-529-9788 Sequence 9788, Ap
19	12.4	62.0	25	7	US-11-217-529-23135 Sequence 23135, A
20	12.4	62.0	25	7	US-11-217-529-117896 Sequence 117896, A
21	12.4	62.0	34	6	US-10-946-650-26 Sequence 26, Appl
22	12.2	61.0	21	7	US-11-264-784-183 Sequence 183, Appl
23	12.2	61.0	25	7	US-11-217-529-9472 Sequence 9472, Ap
24	12.2	61.0	25	7	US-11-217-529-28702 Sequence 28702, A
25	12.2	61.0	25	7	US-11-217-529-33496 Sequence 33496, A

c	26	12.2	61.0	25	7	US-11-217-529-59585	Sequence 59585, A
	27	12.2	61.0	25	7	US-11-217-529-65432	Sequence 65432, A
	28	12.2	61.0	25	7	US-11-217-529-67969	Sequence 67969, A
c	29	12.2	61.0	25	7	US-11-217-529-94140	Sequence 94140, A
	30	12.2	61.0	25	7	US-11-217-529-179468	Sequence 179468, A
	31	12.2	61.0	50	6	US-10-511-937-42	Sequence 42, Appl
	32	12	60.0	21	7	US-11-078-073-598	Sequence 598, App
	33	12	60.0	23	7	US-11-078-073-321	Sequence 321, App
	34	12	60.0	23	7	US-11-078-073-322	Sequence 322, App
	35	12	60.0	23	7	US-11-078-073-323	Sequence 323, App
	36	12	60.0	23	7	US-11-078-073-324	Sequence 324, App
c	37	12	60.0	23	7	US-11-078-073-599	Sequence 599, App
	38	12	60.0	25	7	US-11-217-529-9790	Sequence 9790, Ap
	39	12	60.0	25	7	US-11-217-529-11244	Sequence 11244, A
c	40	12	60.0	25	7	US-11-217-529-41621	Sequence 41621, A
	41	12	60.0	25	7	US-11-217-529-42036	Sequence 42036, A
c	42	12	60.0	25	7	US-11-217-529-122597	Sequence 122597, A
	43	12	60.0	25	7	US-11-217-529-134018	Sequence 134018, A
	44	12	60.0	30	1	US-09-756-0978-91	Sequence 91, Appl
c	45	11.8	59.0	25	7	US-11-217-529-17865	Sequence 17865, A

#### ALIGNMENTS

RESULT 1  
US-11-217-529-23140  
; Sequence 23140, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 23140  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-23140  
Query Match 77.0%; Score 15.4; DB 7; Length 25;  
Best Local Similarity 94.1%; Pred. No. 6;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 GCTAACATCTCCAAGTC 20  
|||||  
Db 5 GCTAAGATCTCCAAGTC 21  
RESULT 2  
US-11-217-529-107428  
; Sequence 107428, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529

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/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 107428
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-107428

Query Match          76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 7.7;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTTAACATCTCCAAGTC 20
Db 5 GGTGCTAAGATCACCAAGTC 24

RESULT 3
US-11-217-529-35122
/ Sequence 35122, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 35122
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-35122

Query Match          70.0%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AACATCTCCAAGTC 20
Db 4 AACATCTCCAAGTC 17

RESULT 4
US-11-217-529-70037
/ Sequence 70037, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3

/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 70037
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-70037

Query Match          69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTTAACATCTCCAAG 18
Db 3 GAGCTGACATCTTCAAG 19

RESULT 5
US-11-217-529-85327
/ Sequence 85327, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 85327
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-85327

Query Match          69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAAGTC 20
Db 6 GCTGACATCTCCAAGCC 22

RESULT 6
US-11-217-529-46511
/ Sequence 46511, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 46511
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-46511
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Query Match 58.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 51;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGAGCTAAACATCTCCCAAGTC 20  
||| ||||| ||||| |||||  
DB 1 GGAACTAACACCTGCCAAGGC 20

## RESULT 7

US-11-217-529-134913/c  
; Sequence 134913, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 134913  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-134913

Query Match 66.0%; Score 13.2; DB 7; Length 25;  
Best Local Similarity 83.3%; Pred. No. 82;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCTAAACATCTCCCAAGT 19  
||| ||||| ||||| |||||  
DB 23 GAGAAACATGCCCAAGT 6

## RESULT 8

US-11-217-529-8091/c  
; Sequence 8091, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 8091  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-8091

Query Match 64.0%; Score 12.8; DB 7; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGCTAACATCTCCAAG 18  
||| ||||| ||||| |||||  
DB 19 AGGTAAACATCACCAG 4

## RESULT 9

US-11-217-529-191839/c  
; Sequence 191839, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 191839  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-191839

Query Match 64.0%; Score 12.8; DB 7; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGCTAACATCTCCAAG 18  
||| ||||| ||||| |||||  
DB 21 AGCTAACACGCTACAAG 6

## RESULT 10

US-10-511-937-2714/c  
; Sequence 2714, Application US/10511937  
; Publication No. US20060088836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2714  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-511-937-2714

Query Match 64.0%; Score 12.8; DB 6; Length 50;  
Best Local Similarity 87.5%; Pred. No. 1.5e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAGCTAACATCTCCAA 17  
|||||  
Db 32 GAGCTAATATCTCAA 17  
|||||

## RESULT 11

US-11-217-529-46927  
; Sequence 46927, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 46927  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-46927

Query Match 63.0%; Score 12.6; DB 7; Length 25;  
Best Local Similarity 78.9%; Pred. No. 1.7e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGAGCTAACATCTCCAAGT 19  
|||||  
Db 2 GAAGCTGGCTTCTCCAAGT 20  
|||||

## RESULT 12

US-11-217-529-84789  
; Sequence 84789, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 84789  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-84789

Query Match 63.0%; Score 12.6; DB 7; Length 25;  
Best Local Similarity 78.9%; Pred. No. 1.7e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGAGCTAACATCTCCAAGT 19  
|||||  
Db 5 GGATCTAACCTCACTAAGT 23  
|||||

## RESULT 13

US-11-217-529-129113/c  
; Sequence 129113, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 129113  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-129113

Query Match 63.0%; Score 12.6; DB 7; Length 25;  
Best Local Similarity 78.9%; Pred. No. 1.7e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GAGCTAACATCTCCAAGTC 20  
|||||  
Db 19 GAGATAAATTTTCAAGTC 1  
|||||

## RESULT 14

US-11-217-529-141646/c  
; Sequence 141646, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 141646  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-141646

Query Match 63.0%; Score 12.6; DB 7; Length 25;  
Best Local Similarity 78.9%; Pred. No. 1.7e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GAGCTAACATCTCCAAGTC 20  
|||||  
Db 23 GAGCCAGCATGTCCTCAATTC 5  
|||||

## RESULT 15

US-11-217-529-170895/c  
; Sequence 170895, Application US/11217529

; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 170895  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-170895

Query Match 63.0%; Score 12.6; DB 7; Length 25;  
Best Local Similarity 78.9%; Pred.No. 1.7e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GAGCTAACATCTCCAGTC 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 21 GTGCTCTCATCTCCAGTC 3

Search completed: May 21, 2006, 22:34:13  
Job time : 33.5 secs

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:09:23 ; Search time 1331 Seconds  
(without alignments)  
960.893 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggagctaacatctccaagtc 20

Scoring table: IDENTITY\_NUC

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Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb\_pat.\*

3: gb\_ph.\*

4: gb\_pl.\*

5: gb\_pr.\*

6: gb\_ro.\*

7: gb\_sta.\*

8: gb\_sy.\*

9: gb\_un.\*

10: gb\_vl.\*

11: gb\_ov.\*

12: gb\_htg.\*

13: gb\_in.\*

14: gb\_om.\*

15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 4	20	100.0	58	2	BD187058
5	20	100.0	58	2	BD187066
C 6	20	100.0	60	2	CQ536778
C 7	20	100.0	66	2	BD187057
C 8	20	100.0	66	2	BD187065
C 9	20	100.0	168	2	BD187042
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C 24	20	100.0	2537	5	AF207602
C 25	20	100.0	2551	14	AB018398
C 26	20	100.0	3013	14	AY971808
C 27	20	100.0	3229	2	AR531606
C 28	20	100.0	3296	14	AY621118
C 29	20	100.0	3551	5	AB073325
C 30	20	100.0	3669	5	AB169332
C 31	20	100.0	3678	2	AR367892
C 32	20	100.0	3678	2	AR642334
C 33	20	100.0	3678	2	AX504300
C 34	20	100.0	3678	2	AX770508
C 35	20	100.0	3678	5	HSU22431
C 36	20	100.0	3736	2	BD222980
C 37	20	100.0	3736	2	AR317244
C 38	20	100.0	3913	2	CQ719027
C 39	20	100.0	3927	2	AX321214
C 40	20	100.0	3933	2	AX763546
C 41	20	100.0	3933	5	BC012527
C 42	20	100.0	3933	5	HSU29165
C 43	20	100.0	3945	5	HSM808946
C 44	20	100.0	3958	2	CS097358
C 45	20	100.0	7059	2	BD187076

#### ALIGNMENTS

BD187062 49 bp DNA linear PAT 17-JUN-2003  
Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.

BD187062  
BD187062.1 GI:31879262  
WO 02099104-A/22.  
synthetic construct  
other sequences; artificial sequences.  
1 (bases 1 to 49)  
Hiraoka, M., Kondo, S. and Harada, H.  
Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it  
Patent: WO 02099104-A 22 12-DEC-2002;  
POLA CHEMICAL INDUSTRIES INC.MASAHIRO HIRAOKA,SHINAE KONDO, HIROSHI HARADA

OS Artificial Sequence  
PN WO 02099104-A/22  
PD 12-DEC-2002  
PF 04-JUN-2002 WO 2002JP005482  
PR 05-JUN-2001 JP 01P 169948, 05-JUN-2001 JP 01P 169949 PI  
PC C12N15/09.C1201/68.C07K14/47.C07K19/00  
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source

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BD187041/c
LOCUS
DEFINITION
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it.
PAT 17-JUN-2003
ACCESSION
BD187041
VERSION
BD187041.1 GI:31879241
KEYWORDS
WO 02099104-A/1.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 54)
AUTHORS
Hiraoka,M., Kondo,S. and Harada,H.
TITLE
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it
JOURNAL
Patent: WO 02099104-A 1 12-DEC-2002;
POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAOKA,SHINAE KONDO, HIROSHI
HARADA
COMMENT
OS Artificial Sequence
PN WO 02099104-A/1
PD 12-DEC-2002
PF 04-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
MASAHIRO HIRAOKA,SHINAE KONDO,HIROSHI HARADA
PC C12N15/09,C12Q1/68,C07K14/47,C07K19/00
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Db 28 GGAGCTAACATCTCCAAGTC 9

RESULT 4
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LOCUS
DEFINITION
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it.
PAT 17-JUN-2003
ACCESSION
BD187058
VERSION
BD187058.1 GI:31879258
KEYWORDS
WO 02099104-A/18.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 58)
AUTHORS
Hiraoka,M., Kondo,S. and Harada,H.
TITLE
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it
JOURNAL
Patent: WO 02099104-A 18 12-DEC-2002;
POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAOKA,SHINAE KONDO, HIROSHI
HARADA
COMMENT
OS Artificial Sequence
PN WO 02099104-A/18
PD 12-DEC-2002
PF 04-JUN-2002 WO 2002JP005482
PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
MASAHIRO HIRAOKA,SHINAE KONDO,HIROSHI HARADA
PC C12N15/09,C12Q1/68,C07K14/47,C07K19/00
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Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 35 GGAGCTAACATCTCCAAGTC 54

RESULT 5
BD187066
LOCUS
DEFINITION
Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it.
PAT 17-JUN-2003
ACCESSION
BD187066
VERSION
BD187066.1 GI:31879266

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KEYWORDS      WO 02099104-A/26.
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1 (bases 1 to 58)
AUTHORS      Hiraoka,M., Kondo,S. and Harada,H.
TITLE        Polypeptide causing protein unstable in cell under aerobic
JOURNAL      condition and DNA encoding it
              Patent: WO 02099104-A 26 12-DEC-2002;
              POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAKA,SHINAE KONDO, HIROSHI
              HARADA
COMMENT       OS Artificial Sequence
              PN WO 02099104-A/26
              PD 12-DEC-2002
              PF 04-JUN-2002 WO 2002JP005482
              PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
              MASAHIRO HIRAKA,SHINAE KONDO,HIROSHI HARADA
              PC C12N15/09,C12Q1/68,C07K14/47,C07K19/00
              CC Description of Artificial Sequence: synthetic DNA FH Key
              Location/Qualifiers
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 35 GGAGCTAACATCTCCCAAGTC 54

RESULT 6
LOCUS      CQ536778/c
DEFINITION Sequence 6413 from Patent W00210449.
ACCESSION CQ536778
VERSION   CQ536778.1 GI:41503042
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homnidae; Homo.
REFERENCE  1
AUTHORS   Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE     Oligonucleotide library for detecting rna transcripts and splice
JOURNAL   variants that populate a transcriptome
          Patent: WO 0210449-A 6413 07-FEB-2002;
          Compugen Inc. (US)
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 51 GGAGCTAACATCTCCCAAGTC 32

RESULT 7

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BD187057/c
LOCUS      BD187057
DEFINITION Polypeptide causing protein unstable in cell under aerobic
              condition and DNA encoding it.
ACCESSION BD187057
VERSION   BD187057.1 GI:31879257
KEYWORDS  WO 02099104-A/17.
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 66)
AUTHORS   Hiraoka,M., Kondo,S. and Harada,H.
TITLE     Polypeptide causing protein unstable in cell under aerobic
              condition and DNA encoding it
JOURNAL   Patent: WO 02099104-A 17 12-DEC-2002;
              POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAKA,SHINAE KONDO, HIROSHI
              HARADA
COMMENT       OS Artificial Sequence
              PN WO 02099104-A/17
              PD 12-DEC-2002
              PF 04-JUN-2002 WO 2002JP005482
              PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
              MASAHIRO HIRAKA,SHINAE KONDO,HIROSHI HARADA
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCCAAGTC 20
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Db 28 GGAGCTAACATCTCCCAAGTC 9

RESULT 8
LOCUS      BD187065/c
DEFINITION Polypeptide causing protein unstable in cell under aerobic
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ACCESSION BD187065
VERSION   BD187065.1 GI:31879265
KEYWORDS  WO 02099104-A/25.
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 66)
AUTHORS   Hiraoka,M., Kondo,S. and Harada,H.
TITLE     Polypeptide causing protein unstable in cell under aerobic
              condition and DNA encoding it
JOURNAL   Patent: WO 02099104-A 25 12-DEC-2002;
              POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAKA,SHINAE KONDO, HIROSHI
              HARADA
COMMENT       OS Artificial Sequence
              PN WO 02099104-A/25
              PD 12-DEC-2002
              PF 04-JUN-2002 WO 2002JP005482
              PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
              MASAHIRO HIRAKA,SHINAE KONDO,HIROSHI HARADA
              PC C12N15/09,C12Q1/68,C07K14/47,C07K19/00
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Db 28 GGAGCTAACATCTCCAAGTC 9

RESULT 9
BD187042/c
LOCUS BD187042
DEFINITION Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it.
ACCESSION BD187042
VERSION 1 GI:31879242
KEYWORDS WO 02099104-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 168)
AUTHORS Hiraoka,M., Kondo,S. and Harada,H.
TITLE Polypeptide causing protein unstable in cell under aerobic
condition and DNA encoding it
JOURNAL Patent: WO 02099104-A 2 12-DEC-2002;
POLA CHEMICAL INDUSTRIES INC,MASAHIRO HIRAOKA,SHINAE KONDO, HIROSHI
HARADA
COMMENT OS Artificial Sequence
PN WO 02099104-A/2
PD 12-DEC-2002
PF 04-JUN-2002 WO 2002JP005482
PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI
MASAHIRO HIRAOKA,SHINAE KONDO,HIROSHI HARADA
PC C12N15/09,C12Q1/68,C07K14/47,C07K19/00
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 50 GGAGCTAACATCTCCAAGTC 31

RESULT 10
AY843289S6/c
LOCUS AY843289S6
DEFINITION Phoca hispida hypoxia-inducible factor 1alpha gene, exons 11, 12
and partial cds.
ACCESSION AY843289
VERSION 1 GI:61652850
KEYWORDS 6 of 7
SEGMENT Phoca hispida (ringed seal)
SOURCE Phoca hispida
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Carnivora; Pinnipedia;
Phocidae; Phoca.
1 (bases 1 to 716)
Johnson,P., Elsner,R. and Zenteno-Savin,T.
Hypoxia-Inducible Factor in Ringed Seal (Phoca hispida) tissues
Free Radic. Res. 38 (8), 847-854 (2004)
15493458
2 (bases 1 to 716)
Johnson,P., Elsner,R. and Zenteno-Savin,T.
Hypoxia-inducible factor 1 proteomics and diving adaptations in
ringed seal
Free Radic. Biol. Med. 39 (2), 205-212 (2005)
15964512
3 (bases 1 to 716)
Johnson,P., Elsner,R. and Zenteno-Savin,T.
Direct Submission
Submitted (01-DEC-2004) Biomedical Sciences, Ohio University,
Irvine Hall, Athens, OH 45701, USA
Location/Qualifiers
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/number=12

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Db 372 GGAGCTAACATCTCCAAGTC 353

RESULT 11
HSHIF1A10/c
LOCUS HSHIF1A10
DEFINITION Homo sapiens hypoxia-inducible factor 1 alpha subunit (HIF1A) gene,
exons 11 and 12.
ACCESSION AF050124
VERSION AF050124.1 GI:3790530
KEYWORDS 10 of 13
SEGMENT Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 996)
Iyer,N.V., Leung,S.W. and Semenza,G.L.
The human hypoxia-inducible factor 1alpha gene: HIF1A structure and
evolutionary conservation
Genomics 52 (2), 159-165 (1998)
9782081
2 (bases 1 to 996)
Iyer,N.V., Leung,S.W. and Semenza,G.L.
Direct Submission
Submitted (24-FEB-1998) Departments of Pediatrics and Medicine,

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Institute of Genetic Medicine, Johns Hopkins University School of Medicine, 600 N. Wolfe St, Baltimore, MD 21287-3914, USA

# FEATURES

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469..902  
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## ORIGIN

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DB 500 GGAGCTAACATCTCCAAGTC 481

## RESULT 12

AX147413/c  
LOCUS AX147413 1335 bp DNA linear PAT 08-JUN-2001  
DEFINITION Sequence 1 from Patent WO0136616.  
ACCESSION AX147413  
VERSION AX147413.1 GI:14346570

KEYWORDS  
SYNTHETIC CONSTRUCT  
OTHER SEQUENCES; artificial sequences.

## REFERENCE

1  
Beuzard, Y., Payen, E., Scherman, D. and Bettan, M.  
Acid nucleic construct bearing a system regulating the expression of a gene  
Patent: WO 0136616-A 1 25-MAY-2001;  
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR) ; Aventis Pharma S.A. (FR)

## FEATURES

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DB 749 GGAGCTAACATCTCCAAGTC 730

## RESULT 13

AY455802/c  
LOCUS AY455802 2359 bp mRNA linear MAM 23-NOV-2003  
DEFINITION Canis familiaris hypoxia-inducible factor 1 alpha subunit mRNA,  
partial cds.

ACCESSION AY455802  
VERSION AY455802.1 GI:38374004  
KEYWORDS  
Canis familiaris (dog)  
Canis familiaris  
ORGANISM

## REFERENCE

1 (bases 1 to 2359)  
Spee, B., Penning, L.C. and Rothuizen, J.  
Differential gene expression of regenerative and fibrotic pathways in canine hepatic portosystemic shunt and portal vein hypoplasia  
Unpublished  
2 (bases 1 to 2359)  
Spee, B., Penning, L.C. and Rothuizen, J.  
Direct Submission  
Submitted (31-OCT-2003) Dept. of Clinical Sciences of Companion Animals, University Utrecht, Yalelaan 8, Utrecht, UTR 3508TD, Netherlands

## FEATURES

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## ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 2359;  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.8  
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Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggagtaacatctcaagtc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq 8:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

14: Geneseqn2005s:\*

15: Geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	20	13	ADQ88723
C 2	20	100.0	20	13	ADQ88724
C 3	20	100.0	49	8	ABZ76611 Human HIF
C 4	20	100.0	54	8	ABZ71164 Hypoxia-i
C 5	20	100.0	57	8	ABZ76610 Human HIF
C 6	20	100.0	58	8	ABZ76615 Human HIF
C 7	20	100.0	58	8	ABZ76607 Human HIF
C 8	20	100.0	60	6	ABN33665 Human spl
C 9	20	100.0	66	8	ABZ71180 Human HIF
C 10	20	100.0	66	8	ABZ76614 Human HIF
C 11	20	100.0	168	8	ABZ71165 Nucleotid
C 12	20	100.0	1335	4	Aaf85323
C 13	20	100.0	1354	14	ABEC31706
C 14	20	100.0	2481	6	ABV78154 Human HIF
C 15	20	100.0	2481	6	ABZ35730 Human HIF
C 16	20	100.0	2481	6	ABK11552 Human CDN
C 17	20	100.0	2481	6	ABX09973 Human HIF
C 18	20	100.0	2481	6	ABL91695 Human pol

C 19	20	100.0	2487	5	AAS85055	Aas85055 DNA encod
C 20	20	100.0	2517	8	ACC59243	ACC59243 Human HIF
C 21	20	100.0	2528	4	AAS14154	Aas14154 Human HIF
C 22	20	100.0	2528	6	AAD45951	Aad45951 Human hyp
C 23	20	100.0	2528	10	ADD19045	Add19045 HIF-1alp
C 24	20	100.0	2861	6	ABQ54551	Abq54551 Human ova
C 25	20	100.0	3203	12	AD116279	Ad116279 Human nuc
C 26	20	100.0	3229	9	ADA24506	Ada24506 Human CDN
C 27	20	100.0	3229	10	ADJ56307	Adj56307 Human CDN
C 28	20	100.0	3229	10	ADJ56307	Adj56307 Human CDN
C 29	20	100.0	3229	12	ADJ56307	Adj56307 Human CDN
C 30	20	100.0	3551	12	ADJ56307	Adj56307 Human CDN
C 31	20	100.0	3551	13	ADT78443	Adt78443 Human HIF
C 32	20	100.0	3678	2	AAV63210	Aav63210 Nucleic a
C 33	20	100.0	3678	6	AAV63210	Aav63210 Nucleic a
C 34	20	100.0	3678	6	ABK84267	Abk84267 Human CDN
C 35	20	100.0	3678	8	ACA89893	Aca89893 Gene diff
C 36	20	100.0	3678	10	ABZ83187	Abz83187 Toxicolog
C 37	20	100.0	3678	14	AED17984	Aed17984 Fibrotic
C 38	20	100.0	3736	2	AAT45937	Aat45937 Human hyp
C 39	20	100.0	3736	3	AZ299537	Aaz299537 DNA encod
C 40	20	100.0	3736	9	ADA18530	Ada18530 Human DNA
C 41	20	100.0	3736	14	AEC09680	Aec09680 Human HIF
C 42	20	100.0	3812	12	ADO26976	Ado26976 Human HIF
C 43	20	100.0	3927	6	AAS61690	Aas61690 Lung smal
C 44	20	100.0	3933	2	AAx58980	Aax58980 Human tra
C 45	20	100.0	3933	8	ADA03184	Ada03184 Human Hif

ALIGNMENTS

RESULT 1

ADQ88723/c

ID ADQ88723 standard; DNA; 20 BP.

XX

AC ADQ88723;

XX

DT 21-OCT-2004 (first entry)

XX Human hypoxia inducible factor-1 gene fragment seqid 2.

XX RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;

KW cancer; infection; inflammation; tumour formation; ss.

XX Homo sapiens.

OS

XX US2004152655-A1.

PN

XX 05-AUG-2004.

PD

PF 28-JAN-2004; 2004US-00766185.

PP

XX 31-JAN-2003; 2003US-0444367P.

PR

XX

PA (YOON/) YOON H.

PA (MAOL/) MAO L.

PA (LEEV/) LEE Y B.

PA (AHNC/) AHN C.

PA (JIAN/) JIANG X.

XX

PI Yoon H, Mao L, Lee YB, Ahn C, Jiang X;

XX

DR WPI; 2004-561492/54.

XX

PT New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a

PT nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),

PT useful for inhibiting expression of HIF-1 and inducing cytotoxicity in

PT several cancer cells.

XX

XX Example 4; SEQ ID NO 3; 35pp; English.

XX

CC The invention describes a compound, RX-0047 or RX-0149 targeted to a

CC nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),  
 CC where the oligonucleotide compound inhibits the expression of human HIF-  
 CC 1. Also described are: a method of inhibiting the expression of human HIF-1 in  
 CC human cells or tissues; and a method of inducing cytotoxicity in a cancer  
 CC cell. Specifically claimed are RX-0047 and RX-0149 compounds having a  
 CC fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5,  
 CC aatgagccaccagtgctcaa 3' and SEQ ID NO. 4, 5', ggagctaacatctcccaagtc 3',  
 CC respectively). The compounds are useful for inhibiting the expression of  
 CC HIF-1 and inducing the cytotoxicity in several cancer cells. The  
 CC antisense compounds are also useful for preventing or delaying infection,  
 CC inflammation, or tumour formation. This sequence represents a site on the  
 CC HIF-1 to which antisense oligonucleotides can be targetted in order to  
 CC control HIF-1 gene expression.

XX  
 SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 13; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.7;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20  
 DB 20 GGAGCTAACATCTCCCAAGTC 1

RESULT 2  
 ADQ88724  
 ID ADQ88724 standard; DNA; 20 BP.  
 AC ADQ88724;  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE Human HIF-1 antisense oligonucleotide RX-0149.  
 XX  
 KW RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;  
 KW cancer; infection; inflammation; tumour formation; ss;  
 KW antisense oligonucleotide; antisense technology.

XX Homo sapiens.  
 XX US2004152655-A1.  
 XX 05-AUG-2004.  
 XX 28-JAN-2004; 2004US-00766185.  
 XX 31-JAN-2003; 2003US-0444367P.  
 XX (YOON/) YOON H.  
 XX (MAOL/) MAO L.  
 XX (LEEY/) LEE Y B.  
 XX (AHNC/) AHN C.  
 XX (JIAN/) JIANG X.  
 XX Yoon H, Mao L, Lee YB, AHN C, JIANG X;  
 XX WPI; 2004-561492/54.  
 XX  
 XX New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a  
 XX nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),  
 XX useful for inhibiting expression of HIF-1 and inducing cytotoxicity in  
 XX several cancer cells.  
 XX  
 XX Claim 6; SEQ ID NO 4; 35pp; English.

XX The invention describes a compound, RX-0047 or RX-0149 targeted to a  
 XX nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),  
 XX where the oligonucleotide compound inhibits the expression of human HIF-  
 XX 1. Also described are: a method of inhibiting the expression of HIF-1 in  
 XX human cells or tissues; and a method of inducing cytotoxicity in a cancer  
 XX cell. Specifically claimed are RX-0047 and RX-0149 compounds having a  
 XX fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5,

CC aatgagccaccagtgctcaa 3' and SEQ ID NO. 4, 5' ggagctaacatctcccaagtc 3',  
 CC respectively). The compounds are useful for inhibiting the expression of  
 CC HIF-1 and inducing the cytotoxicity in several cancer cells. The  
 CC antisense compounds are also useful for preventing or delaying infection,  
 CC inflammation, or tumour formation. This sequence represents a human HIF-1  
 CC antisense oligonucleotide.

XX  
 SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 13; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.7;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20  
 DB 1 GGAGCTAACATCTCCCAAGTC 20

RESULT 3  
 ABZ76611  
 ID ABZ76611 standard; DNA; 49 BP.  
 XX  
 AC ABZ76611;

DT 30-APR-2003 (first entry)

DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:24.

XX  
 KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;  
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;  
 KW tumour; nuclear localisation signal; oxygen dependent degradation domain;  
 KW NLS; ODD; PCR primer; ss.

XX Homo sapiens.

XX WO200299104-A1.

XX 12-DEC-2002.

XX 04-JUN-2002; 2002WO-JP005482.

XX 05-JUN-2001; 2001JP-00169948.

XX 05-JUN-2001; 2001JP-00169949.

XX (POKK) POLA CHEM IND INC.

XX (HIRA/) HIRAKA M.

XX (KOND/) KONDOH S.

XX Hiraoka M, Kondoh S, Harada H;

XX WPI; 2003-148670/14.

XX  
 PT New DNA encoding a polypeptide imparting relative stability under hypoxic  
 PT conditions to proteins within the cell, useful for treatment of cancer  
 PT and improvement of microbial fermentation.

XX Example; Page 24; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1  
 XX alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAFYIPMDDDFQL  
 XX see ABP57669) (I), or encoding a fusion protein containing at least 16  
 XX residues of (I), a nuclear localisation signal (NLS), and another  
 XX protein, and imparting relative stability under specific conditions of  
 XX oxygen concentration within the cell. Also described: (1) vectors  
 XX containing the DNA; (2) cells transformed by the vectors; (3) producing  
 XX the fusion protein by culture of the transformed cells; (4) detecting  
 XX hypoxic conditions in cells by monitoring the stability of the protein  
 XX fused to (I) in cells transformed by vectors containing the DNA; (5)  
 XX regulating the stability of proteins within the cell by transformation  
 XX with the DNA; (6) inhibiting the development of cells under hypoxic  
 XX conditions, using the fusion protein; (7) fusion proteins encoded by the  
 XX DNA; and (8) stabilisation of cells under specific conditions of oxygen  
 XX tension. (I) has cytostatic activity, and can be used for the

CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a  
 CC solid tumour, and in gene therapy. (1) can be used in industrial  
 CC microbial fermentation, and in medicine, especially in the treatment of  
 CC tumours containing hypoxic regions. The present sequence represents a PCR  
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)  
 CC domain, which is used in an example from the present invention  
 XX

SQ Sequence 49 BP; 15 A; 11 C; 10 G; 13 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 8; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 3;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20  
 |||||  
 Db 26 GGAGCTAACATCTCCAAGTC 45

## RESULT 4

ABZ71164/c  
 ID ABZ71164 standard; DNA; 54 BP.

XX AC ABZ71164;

XX DT 30-APR-2003 (first entry)

XX DE Hypoxia-inducible factor 1 alpha 557-574 peptide encoding DNA SEQ.2.

XX KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;  
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;  
 KW tumour; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 1..54

FT /tag= a

FT /partial

FT /product= "HIF-1 alpha 557-574 peptide"

FT /note= "no start or stop codons given"

XX PN WO200299104-A1.

XX PD 12-DEC-2002.

XX PF 04-JUN-2002; 2002WO-JP005482.

XX PR 05-JUN-2001; 2001JP-00169948.

XX PR 05-JUN-2001; 2001JP-00169949.

XX PA (POKK ) POLA CHEM IND INC.

XX PA (HIRA/) HIRAOKA M.

XX PA (KOND/) KONDOH S.

XX PI Hiraoka M, Kondoh S, Harada H;

XX WPI; 2003-148670/14.

DR P-PSDB; ABP57669.

XX PT New DNA encoding a polypeptide imparting relative stability under hypoxic  
 PT conditions to proteins within the cell, useful for treatment of cancer  
 PT and improvement of microbial fermentation.

XX PS Claim 3; Page 58; 144pp; Japanese.

XX CC The present invention describes DNA encoding a hypoxia-inducible factor 1  
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL  
 CC see ABP57669) (1), or encoding a fusion protein containing at least 16  
 CC residues of (1), a nuclear localisation signal (NLS), and another  
 CC protein, and imparting relative stability under specific conditions of  
 CC oxygen concentration within the cell. Also described: (1) vectors  
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing  
 CC the fusion protein by culture of the transformed cells; (4) detecting

CC hypoxic conditions in cells by monitoring the stability of the protein  
 CC fused to (1) in cells transformed by vectors containing the DNA; (5)  
 CC regulating the stability of proteins within the cell by transformation  
 CC with the DNA; (6) inhibiting the development of cells under hypoxic  
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the  
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen  
 CC tension. (1) has cytostatic activity, and can be used for the  
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a  
 CC solid tumour, and in gene therapy. (1) can be used in industrial  
 CC microbial fermentation, and in medicine, especially in the treatment of  
 CC tumours containing hypoxic regions. The present sequence encodes (1) from  
 XX the present invention

SQ Sequence 54 BP; 14 A; 11 C; 11 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20

|||||  
 Db 23 GGAGCTAACATCTCCAAGTC 4

## RESULT 5

ABZ76610/c

ID ABZ76610 standard; DNA; 57 BP.

XX AC ABZ76610;

XX DT 30-APR-2003 (first entry)

XX DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:23.

XX KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;  
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;  
 KW tumour; nuclear localisation signal; oxygen dependent degradation domain;  
 KW NLS; ODD; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200299104-A1.

XX PD 12-DEC-2002.

XX PF 04-JUN-2002; 2002WO-JP005482.

XX PR 05-JUN-2001; 2001JP-00169948.

XX PR 05-JUN-2001; 2001JP-00169949.

XX PA (POKK ) POLA CHEM IND INC.

XX PA (HIRA/) HIRAOKA M.

XX PA (KOND/) KONDOH S.

XX PI Hiraoka M, Kondoh S, Harada H;

XX WPI; 2003-148670/14.

XX PT New DNA encoding a polypeptide imparting relative stability under hypoxic  
 PT conditions to proteins within the cell, useful for treatment of cancer  
 PT and improvement of microbial fermentation.

XX PS Example; Page 24; 144pp; Japanese.

XX CC The present invention describes DNA encoding a hypoxia-inducible factor 1  
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL  
 CC see ABP57669) (1), or encoding a fusion protein containing at least 16  
 CC residues of (1), a nuclear localisation signal (NLS), and another  
 CC protein, and imparting relative stability under specific conditions of  
 CC oxygen concentration within the cell. Also described: (1) vectors  
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing  
 CC the fusion protein by culture of the transformed cells; (4) detecting  
 CC hypoxic conditions in cells by monitoring the stability of the protein

CC fused to (1) in cells transformed by vectors containing the DNA; (5)  
 CC regulating the stability of proteins within the cell by transformation  
 CC with the DNA; (6) inhibiting the development of cells under hypoxic  
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the  
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen  
 CC tension. (1) has cytostatic activity, and can be used for the  
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a  
 CC solid tumour, and in gene therapy. (1) can be used in industrial  
 CC microbial fermentation, and in medicine, especially in the treatment of  
 CC tumours containing hypoxic regions. The present sequence represents a PCR  
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)  
 CC domain, which is used in an example from the present invention  
 XX  
 SQ Sequence 57 BP; 15 A; 12 C; 13 G; 17 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 3.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAGCTAACATCTCCAAGTC 20  
 |||||  
 Db 28 GGAGCTAACATCTCCAAGTC 9

RESULT 6  
 ABZ76615  
 ID ABZ76615 standard; DNA; 58 BP.

AC ABZ76615;  
 DT 30-APR-2003 (first entry)

DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:28.

KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;  
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;  
 KW tumour; nuclear localisation signal; oxygen dependent degradation domain;  
 KW NLS; ODD; PCR primer; ss.

OS Homo sapiens.

PN WO200299104-A1.

PD 12-DEC-2002.

PF 04-JUN-2002; 2002WO-JP005482.

PR 05-JUN-2001; 2001JP-00169948.

PR 05-JUN-2001; 2001JP-00169949.

PA (POKK) POLA CHEM IND INC.

PA (HIRA/) HIRAOKA M.

PA (KOND/) KONDOH S.

PI Hiraoka M, Kondoh S, Harada H;

DR WPI; 2003-148670/14.

PT New DNA encoding a polypeptide imparting relative stability under hypoxic  
 PT conditions to proteins within the cell, useful for treatment of cancer  
 PT and improvement of microbial fermentation.

PS Example; Page 24; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1  
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLARYIPMDDDFQL  
 CC see ABP57669) (1), or encoding a fusion protein containing at least 16  
 CC residues of (1), a nuclear localisation signal (NLS), and another  
 CC protein, and imparting relative stability under specific conditions of  
 CC oxygen concentration within the cell. Also described: (1) vectors  
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing  
 CC the fusion protein by culture of the transformed cells; (4) detecting  
 CC hypoxic conditions in cells by monitoring the stability of the protein

CC fused to (1) in cells transformed by vectors containing the DNA; (5)  
 CC regulating the stability of proteins within the cell by transformation  
 CC with the DNA; (6) inhibiting the development of cells under hypoxic  
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the  
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen  
 CC tension. (1) has cytostatic activity, and can be used for the  
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a  
 CC solid tumour, and in gene therapy. (1) can be used in industrial  
 CC microbial fermentation, and in medicine, especially in the treatment of  
 CC tumours containing hypoxic regions. The present sequence represents a PCR  
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)  
 CC domain, which is used in an example from the present invention  
 XX  
 SQ Sequence 58 BP; 18 A; 13 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 3.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAGCTAACATCTCCAAGTC 20  
 |||||  
 Db 35 GGAGCTAACATCTCCAAGTC 54

RESULT 7  
 ABZ76607

ID ABZ76607 standard; DNA; 58 BP.

AC ABZ76607;

DT 30-APR-2003 (first entry)

DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:20.

KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;  
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;  
 KW tumour; nuclear localisation signal; oxygen dependent degradation domain;  
 KW NLS; ODD; PCR primer; ss.

OS Homo sapiens.

PN WO200299104-A1.

PD 12-DEC-2002.

PF 04-JUN-2002; 2002WO-JP005482.

PR 05-JUN-2001; 2001JP-00169948.

PR 05-JUN-2001; 2001JP-00169949.

PA (POKK) POLA CHEM IND INC.

PA (HIRA/) HIRAOKA M.

PA (KOND/) KONDOH S.

PI Hiraoka M, Kondoh S, Harada H;

DR WPI; 2003-148670/14.

PT New DNA encoding a polypeptide imparting relative stability under hypoxic  
 PT conditions to proteins within the cell, useful for treatment of cancer  
 PT and improvement of microbial fermentation.

PS Example; Page 23; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1  
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLARYIPMDDDFQL  
 CC see ABP57669) (1), or encoding a fusion protein containing at least 16  
 CC residues of (1), a nuclear localisation signal (NLS), and another  
 CC protein, and imparting relative stability under specific conditions of  
 CC oxygen concentration within the cell. Also described: (1) vectors  
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing  
 CC the fusion protein by culture of the transformed cells; (4) detecting  
 CC hypoxic conditions in cells by monitoring the stability of the protein

CC fused to (I) in cells transformed by vectors containing the DNA; (5)  
 CC regulating the stability of proteins within the cell by transfection  
 CC with the DNA; (6) inhibiting the development of cells under hypoxic  
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the  
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen  
 CC tension. (I) has cytostatic activity, and can be used for the  
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a  
 CC solid tumour, and in gene therapy. (I) can be used in industrial  
 CC microbial fermentation, and in medicine, especially in the treatment of  
 CC tumours containing hypoxic regions. The present sequence represents a PCR  
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)  
 CC domain, which is used in an example from the present invention  
 XX  
 SQ Sequence 58 BP; 19 A; 12 C; 12 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 3.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGAGCTAACATCTCCAAGTC 20  
 |||||  
 DB 35 GGAGCTAACATCTCCAAGTC 54

RESULT 8  
 ABN33665/c  
 ID ABN33665 standard; DNA; 60 BP.  
 AC ABN33665;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:6413.  
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200210449-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 20-JUL-2001; 2001WO-IB001903.  
 XX  
 PR 28-JUL-2000; 2000US-0221607P.  
 PR 02-MAY-2001; 2001US-0287724P.  
 XX  
 PA (COMP-) COMPUEN INC.  
 XX  
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX  
 DR WPI; 2002-257383/30.  
 XX  
 PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 XX  
 PS Example 1; SEQ ID NO 6413; 47pp; English.  
 XX

CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridising selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini

CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)  
 XX  
 SQ Sequence 60 BP; 16 A; 16 C; 10 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 3.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGAGCTAACATCTCCAAGTC 20  
 |||||  
 DB 51 GGAGCTAACATCTCCAAGTC 32

RESULT 9  
 ABZ71180/c  
 ID ABZ71180 standard; DNA; 66 BP.  
 AC ABZ71180;  
 XX  
 DT 30-APR-2003 (first entry)  
 XX  
 DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:19.  
 KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;  
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;  
 KW tumour; nuclear localisation signal; oxygen dependent degradation domain;  
 KW NLS; ODD; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200299104-A1.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 04-JUN-2002; 2002WO-JP005482.  
 XX  
 PR 05-JUN-2001; 2001JP-00169948.  
 PR 05-JUN-2001; 2001JP-00169949.  
 XX  
 PA (POKK) POLA CHEM IND INC.  
 PA (HIRA/) HIRAKA M.  
 PA (KOND/) KONDOH S.  
 XX  
 PI Hiraoka M, Kondoh S, Harada H;  
 XX  
 DR WPI; 2003-148670/14.  
 XX  
 PT New DNA encoding a polypeptide imparting relative stability under hypoxic  
 PT conditions to proteins within the cell, useful for treatment of cancer  
 PT and improvement of microbial fermentation.  
 XX  
 PS Example; Page 23; 144pp; Japanese.  
 XX  
 CC The present invention describes DNA encoding a hypoxia-inducible factor 1  
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL  
 CC see ABP57669) (I), or encoding a fusion protein containing at least 16  
 CC residues of (I), a nuclear localisation signal (NLS), and another  
 CC protein, and imparting relative stability under specific conditions of  
 CC oxygen concentration within the cell. Also described: (1) vectors  
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing  
 CC the fusion protein by culture of the transformed cells; (4) detecting  
 CC hypoxic conditions in cells by monitoring the stability of the protein  
 CC fused to (I) in cells transformed by vectors containing the DNA; (5)



CC regulating the stability of proteins within the cell by transformation  
 CC with the DNA; (6) inhibiting the development of cells under hypoxic  
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the  
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen  
 CC tension. (1) has cytostatic activity, and can be used for the  
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a  
 CC solid tumour, and in gene therapy. (1) can be used in industrial  
 CC microbial fermentation, and in medicine, especially in the treatment of  
 CC tumours containing hypoxic regions. The present sequence represents a PCR  
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)  
 CC domain, which is used in an example from the present invention  
 XX  
 SQ Sequence 66 BP; 17 A; 14 C; 14 G; 21 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 3.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20  
 |||||  
 DB 28 GGAGCTAACATCTCCAAGTC 9

RESULT 10  
 ABZ76614/c  
 ID ABZ76614 standard; DNA; 66 BP.

AC ABZ76614;  
 XX  
 DT 30-APR-2003 (first entry)  
 XX  
 DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:27.

XX Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;  
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;  
 KW tumour; nuclear localisation signal; oxygen dependent degradation domain;  
 KW NLS; ODD; PCR primer; ss.

XX Homo sapiens.  
 XX WO200299104-A1.  
 XX 12-DEC-2002.

PF 04-JUN-2002; 2002WO-JP005482.  
 XX  
 PR 05-JUN-2001; 2001JP-00169948.  
 PR 05-JUN-2001; 2001JP-00169949.

XX (POKK ) POLA CHEM IND INC.  
 PA (HIRA/) HIRAOKA M.  
 PA (KOND/) KONDOH S.

XX Hiraoka M, Kondoh S, Harada H;  
 PI  
 XX WPI; 2003-148670/14.

XX New DNA encoding a polypeptide imparting relative stability under hypoxic  
 PT conditions to proteins within the cell, useful for treatment of cancer  
 PT and improvement of microbial fermentation.

XX Example; Page 24; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1  
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPVPMDDDFQL  
 CC see ABZ57669) (1), or encoding a fusion protein containing at least 16  
 CC residues of (1), a nuclear localisation signal (NLS), and another  
 CC protein, and imparting relative stability under specific conditions of  
 CC oxygen concentration within the cell. Also described: (1) vectors  
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing  
 CC the fusion protein by culture of the transformed cells; (4) detecting  
 CC hypoxic conditions in cells by monitoring the stability of the protein  
 CC fused to (1) in cells transformed by vectors containing the DNA; (5)

CC regulating the stability of proteins within the cell by transformation  
 CC with the DNA; (6) inhibiting the development of cells under hypoxic  
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the  
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen  
 CC tension. (1) has cytostatic activity, and can be used for the  
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a  
 CC solid tumour, and in gene therapy. (1) can be used in industrial  
 CC microbial fermentation, and in medicine, especially in the treatment of  
 CC tumours containing hypoxic regions. The present sequence represents a PCR  
 CC primer for the human HIF-1 alpha oxygen dependent degradation (ODD)  
 CC domain, which is used in an example from the present invention  
 XX  
 SQ Sequence 66 BP; 16 A; 15 C; 15 G; 20 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 3.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20  
 |||||  
 DB 28 GGAGCTAACATCTCCAAGTC 9

RESULT 11  
 ABZ71165/c  
 ID ABZ71165 standard; DNA; 168 BP.

AC ABZ71165;  
 XX  
 DT 30-APR-2003 (first entry)  
 XX  
 DE Nucleotide sequence SEQ ID NO:3.

XX Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;  
 KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;  
 KW tumour; gene; ds.

XX Synthetic.  
 XX WO200299104-A1.  
 XX 12-DEC-2002.

PF 04-JUN-2002; 2002WO-JP005482.  
 XX  
 PR 05-JUN-2001; 2001JP-00169948.  
 PR 05-JUN-2001; 2001JP-00169949.

XX (POKK ) POLA CHEM IND INC.  
 PA (HIRA/) HIRAOKA M.  
 PA (KOND/) KONDOH S.

XX Hiraoka M, Kondoh S, Harada H;  
 PI  
 XX WPI; 2003-148670/14.

XX New DNA encoding a polypeptide imparting relative stability under hypoxic  
 PT conditions to proteins within the cell, useful for treatment of cancer  
 PT and improvement of microbial fermentation.

XX Disclosure; Page 59; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1  
 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPVPMDDDFQL  
 CC see ABZ57669) (1), or encoding a fusion protein containing at least 16  
 CC residues of (1), a nuclear localisation signal (NLS), and another  
 CC protein, and imparting relative stability under specific conditions of  
 CC oxygen concentration within the cell. Also described: (1) vectors  
 CC containing the DNA; (2) cells transformed by the vectors; (3) producing  
 CC the fusion protein by culture of the transformed cells; (4) detecting  
 CC hypoxic conditions in cells by monitoring the stability of the protein  
 CC fused to (1) in cells transformed by vectors containing the DNA; (5)  
 CC regulating the stability of proteins within the cell by transformation

CC with the DNA; (6) inhibiting the development of cells under hypoxic  
 CC conditions, using the fusion protein; (7) fusion proteins encoded by the  
 CC DNA; and (8) stabilisation of cells under specific conditions of oxygen  
 CC tension. (I) has cytostatic activity, and can be used for the  
 CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a  
 CC solid tumour, and in gene therapy. (I) can be used in industrial  
 CC microbial fermentation, and in medicine, especially in the treatment of  
 CC tumours containing hypoxic regions. The present sequence represents a  
 CC nucleotide sequence given in the exemplification of the present  
 CC invention. N.B. The present sequence is given in the sequence listing of  
 CC the present invention but is not mentioned further within the  
 CC specification

SQ Sequence 168 BP; 48 A; 44 C; 31 G; 45 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 168;

Best Local Similarity 100.0%; Pred. No. 3.5; Length 168;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20  
 Db 50 GGAGCTAACATCTCCCAAGTC 31

RESULT 12

AAF85323/c  
 ID AAF85323 standard; DNA; 1335 BP.

XX AAF85323;

XX 23-JUL-2001 (first entry)

XX Nucleotide sequence of tRAK-hH104.

XX Nucleic acid construct; oxygen partial pressure; cellular hypoxia;  
 KW anemia; cancer; ischemia; erythropoietin; immunotherapy;  
 KW autoimmune disease; hH104; tRAK; ss.

OS Synthetic.

FH Key Location/Qualifiers

FT CDS 1..1335

PT /\*tag= a

XX WO200136616-A2.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000WO-FR003207.

XX 18-NOV-1999; 99FR-00014513.

XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (AVET ) AVENTIS PHARMA SA.

XX Beuzard Y, Payen E, Scherman D, Bettan M;

XX WPI; 2001-343818/36.

XX P-PSDB; AAB68415.

PT New nucleic acid construct for controlling expression of target gene,  
 PT useful e.g. for treating cancer, is modulated by exogenous  
 PT pharmaceutical and oxygen partial pressure.

XX Disclosure; Page 55-57; 60pp; French.

XX The specification describes a nucleic acid construct bearing a system for  
 CC regulating the expression of a gene. The nucleic acid construct comprises  
 CC at least one sequence encoding a protein that regulates expression of at  
 CC least one gene of interest. The activity of this protein is modulated by  
 CC presence/absence of a pharmacological agent and the amount of protein  
 CC produced depends on the oxygen partial pressure. The constructs are used  
 CC to treat conditions associated with cellular hypoxia, especially anemia,

CC cancer and ischemia, specifically where the gene of interest encodes  
 CC erythropoietin (but many other suitable genes are listed, e.g. those  
 CC encoding single-chain antibodies for immunotherapy of infections or  
 CC autoimmune diseases, prodrug-converting enzymes, apoptosis inducers  
 CC etc.). The present sequence represents the open reading frame of tRAK-  
 CC hH104. The sequence contains a human hH104 fragment, inserted into the  
 CC BstWI site of tRAK. This sequence is used to produce constructs of the  
 CC invention

SQ Sequence 1335 BP; 377 A; 323 C; 323 G; 312 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 1335;

Best Local Similarity 100.0%; Pred. No. 4.5; Length 1335;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20

Db 749 GGAGCTAACATCTCCCAAGTC 730

RESULT 13

AEC31706/c

ID AEC31706 standard; DNA; 1354 BP.

XX AEC31706;

XX 20-OCT-2005 (first entry)

XX Anoxia controlled transcription factor associated DNA, SEQ ID No.1.

XX transcription factor; transcription; anoxia; gene expression; tumor;  
 KW ischemia; heart disease; arthritis; cardiovascular-gen.; cytostatic;  
 KW vasotropic; cardiant; antiarthritic; ds.

XX Unidentified.

XX CN1580262-A.

XX 16-FEB-2005.

XX 12-AUG-2003; 2003CN-00142216.

XX 12-AUG-2003; 2003CN-00142216.

XX (UYSH-) UNIV SHANGHAI NO 3 MEDICAL.

XX Ying LQG, Lu J;

XX WPI, 2005-372977/39.

XX Carrier system containing an artificial transcription factor regulated by  
 PT oxygen deficit, and its configuration and use.

XX Claim 2; SEQ ID NO 1; 27pp; Chinese.

XX The invention relates to a transcription factor controlled by anoxia. The  
 CC transcription factor is produced by a construction method in which GAL4  
 CC DNA combines and HIF1 is active. Also described is a carrier system  
 CC containing the transcription factor of the invention. The system is  
 CC composed of two carriers: (a) one carrier is controlled by anoxia and can  
 CC activate targeted gene expression controlled by the GSTAATA promoter, (b)  
 CC the other carrier contains the GSTAATA promoter. The invention allows the  
 CC displacement of different promoters and the ability of controlling gene  
 CC expression in cells and organisms undergoing anoxia. Different targeted  
 CC genes can be coupled into the carrier for the preparation of therapeutic  
 CC drugs for tumor, ischemia angiodiopathy and arthritis. This sequence  
 CC represents DNA relating to the present invention.

SQ Sequence 1354 BP; 448 A; 267 C; 302 G; 337 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 1354;

Best Local Similarity 100.0%; Pred. No. 4.5; Length 1354;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTTAACATCTCCAAGTC 20  
DB 773 GGAGCTTAACATCTCCAAGTC 754

RESULT 14  
ABV78154/c  
ID ABV78154 standard; DNA; 2481 BP.

XX AC ABV78154;

XX DT 15-NOV-2002 (first entry)

XX DE Human HIF-alpha DNA SEQ ID NO 38.

XX KW RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;  
XX KW virucide; protozoacide; gene; ds.

OS Homo sapiens.

XX PN W0200255693-A2.

XX PD 18-JUL-2002.

XX PF 09-JAN-2002; 2002WO-EP000152.

XX PR 09-JAN-2001; 2001DE-01000586.

XX PR 26-OCT-2001; 2001DE-01055280.

XX PR 29-NOV-2001; 2001DE-01058411.

XX PR 07-DEC-2001; 2001DE-01060151.

XX PA (RIBO-) RIBOPHARMA AG.

XX PI Kreutzer R, Limmer S, Rost S, Hadwiger P;

XX DR WPI; 2002-590671/63.

XX PT Inhibiting expression of target gene, useful e.g. for inhibiting  
PT oncogenes, by administering double-stranded RNA complementary to the  
PT target and having an overhang.

XX PS Claim 10; Page 134-135; 203pp; German.

XX CC The invention relates to inhibiting expression of a target gene (I) in a  
CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded  
CC structure of at most 49 consecutive bases. At least part of one strand  
CC (as1) of dsRNA is complementary to (I) and at least one end of dsRNA  
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the  
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.  
CC in humans, also genes in Plasmodium or in viruses or viroids that are  
CC pathogenic for humans, animals or plants. Introducing an overhang into  
CC dsRNA greatly increases effectiveness for inhibiting gene expression,  
CC both in vivo and in vitro and also increases stability and thus the  
CC effective concentration inside the cell. The present sequence is that of  
CC a gene related to the invention

XX SQ Sequence 2481 BP; 829 A; 512 C; 500 G; 640 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 2481;  
Best Local Similarity 100.0%; Pred. No. 4.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTTAACATCTCCAAGTC 20  
DB 1691 GGAGCTTAACATCTCCAAGTC 1672

RESULT 15  
ABZ35730/c  
ID ABZ35730 standard; DNA; 2481 BP.

XX AC ABZ35730;

XX DT 07-FEB-2003 (first entry)  
XX DE Human HIF-alpha polynucleotide SEQ ID NO 38.

XX KW Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;  
KW protozoacide; gene expression; antisense; tumour; infection; Plasmodium;  
KW virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;  
KW Hepatitis C virus; human papilloma virus; gene; ds.

OS Homo sapiens.

XX PN DE10100588-A1.

XX PD 18-JUL-2002.

XX PF 09-JAN-2001; 2001DE-01000588.

XX PR 09-JAN-2001; 2001DE-01000588.

XX PA (RIBO-) RIBOPHARMA AG.

XX PI Kreutzer R, Limmer S, Rost S, Hadwiger P;

XX DR WPI; 2002-683450/74.

XX PT Inhibiting expression of target genes, useful e.g. for treating tumors,  
PT by introducing into cells two double-stranded RNAs that are complementary  
PT to the target.

XX PS Claim 13; Page 31; 100pp; German.

XX CC The invention relates to inhibiting expression of a target gene in a cell  
CC by introducing at least two oligonucleotides (dsRNAi and II), both  
CC with a double-stranded (ds) structure of at most 49 sequential nucleotide  
CC pairs. At least part of one strand (S1, S2) of the ds structures in each  
CC of dsRNAi and II are complementary to regions in the target gene. The  
CC method uses antisense inhibition of gene expression using double stranded  
CC RNA inhibition (RNAi). The method is particularly used to treat tumours  
CC or infections, especially by Plasmodium or viruses/viroids (pathogenic on  
CC humans, animals or plants). The method provides more effective inhibition  
CC of expression than known methods using a single dsRNA, even at very low  
CC concentrations. When dsRNA has at least one unpaired nucleotide at the  
CC end, stability (and thus effective concentration in the cell) is improved  
CC and efficiency can be increased further by pretreating the cells with  
CC interferon. The present sequence is that of a target DNA of the invention

XX SQ Sequence 2481 BP; 829 A; 512 C; 500 G; 640 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 2481;  
Best Local Similarity 100.0%; Pred. No. 4.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTTAACATCTCCAAGTC 20  
DB 1691 GGAGCTTAACATCTCCAAGTC 1672

Search completed: May 21, 2006, 21:17:45  
Job time : 262.5 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:16:50 ; Search time 2223.5 Seconds  
(without alignments)  
502.985 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 GGAGCTAACTCTCCCAAGTC 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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EST:\*

- 1: gb\_est1:\*
- 2: gb\_est3:\*
- 3: gb\_est4:\*
- 4: gb\_est5:\*
- 5: gb\_est6:\*
- 6: gb\_estc:\*
- 7: gb\_est2:\*
- 8: gb\_est7:\*
- 9: gb\_est8:\*
- 10: gb\_est9:\*
- 11: gb\_est1:\*
- 12: gb\_est2:\*
- 13: gb\_est3:\*
- 14: gb\_est4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	110	2	BF900491
2	20	100.0	165	2	BF734487
3	20	100.0	222	10	T10413
4	20	100.0	316	10	DY178075
5	20	100.0	324	8	CN264306
6	20	100.0	326	7	BE184816
7	20	100.0	357	7	AW860808
8	20	100.0	370	7	AW862545
9	20	100.0	387	10	DY137624
10	20	100.0	400	9	D56430
11	20	100.0	421	7	AW800395
12	20	100.0	421	7	BE856421
13	20	100.0	424	10	DY048267
14	20	100.0	445	7	BE696412
15	20	100.0	453	11	AQ805950
16	20	100.0	454	7	BE696416
17	20	100.0	464	3	BM835867
18	20	100.0	467	9	DA163304
19	20	100.0	470	11	AQ813482

20	20	100.0	472	7	BE696419	QV0-CT038
C 21	20	100.0	486	1	AA937180	KJ3C01.8
C 22	20	100.0	493	3	BM754664	K-EST0032
C 23	20	100.0	495	9	DA699458	DA699458
C 24	20	100.0	503	9	DA551645	DA551645
C 25	20	100.0	514	1	AI921994	WM97C03.X
C 26	20	100.0	522	4	CB267820	C19275820
C 27	20	100.0	528	9	DA653429	1006726.H
C 28	20	100.0	529	9	DA871625	DA653429
C 29	20	100.0	534	9	DB013054	DA871625
C 30	20	100.0	542	9	DA490064	DB013054
C 31	20	100.0	549	9	DA944956	DA490064
C 32	20	100.0	550	9	DA363361	DA944956
C 33	20	100.0	550	9	DA882416	DA363361
C 34	20	100.0	551	9	DA952887	DA882416
C 35	20	100.0	553	9	DA665410	DA952887
C 36	20	100.0	553	9	DA693441	DA665410
C 37	20	100.0	556	9	DA487729	DA693441
C 38	20	100.0	558	9	DA596431	DA487729
C 39	20	100.0	560	9	DA023908	DA596431
C 40	20	100.0	561	9	DA957374	DA023908
C 41	20	100.0	562	8	CN264327	DA957374
C 42	20	100.0	562	9	DA542861	CN264327
C 43	20	100.0	566	8	CN264323	DA542861
C 44	20	100.0	566	9	DA178809	CN264323
C 45	20	100.0	567	9	DA027896	DA178809

#### ALIGNMENTS

RESULT 1  
BF900491  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

BF900491 110 bp mRNA linear EST 18-JAN-2001  
PM1-MT0198-061200-003-c05 MT0198 Homo sapiens cDNA, mRNA sequence.  
BF900491  
BF900491.1 GI:12291950  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 110)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
10737800

JOURNAL  
PUBLISHED

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Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-MT0198-  
061200-003-c05&t3=2000-12-06&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 6  
High quality sequence stop: 110.  
Location/Qualifiers  
1..110  
/organism="Homo sapiens"  
/mol\_type="mRNA"

FEATURES

source

```

/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="WT0198"
/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
    |||||
Db 26 GGAGCTAACATCTCCAAAGTC 45

RESULT 2
LOCUS      BF734487      165 bp      mRNA      linear      EST 09-JAN-2001
DEFINITION PM2-AN0089-081100-011-e04 AN0089 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF734487
VERSION     BF734487.1 GI:12059724
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 165)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED    10737800
COMMENT    Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM2&t2=PM2-AN0089-
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            High quality sequence stop: 164.
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                    /dev_stage="Adult"
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                    /note="Organ: amnion normal; Vector: puc18; Site 1: SmaI;
                    Site 2: SmaI; A mini-library was made by cloning products
                    derived from ORSTES PCR (U.S. Letters Patent application
                    No. 196,716 - Ludwig Institute for Cancer Research)
                    profiles into the pUC 18 vector. Reverse transcription of
                    tissue mRNA and cDNA amplification were performed under
                    low stringency conditions."

ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
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Db 26 GGAGCTAACATCTCCAAAGTC 45

RESULT 2
LOCUS      BF734487      165 bp      mRNA      linear      EST 09-JAN-2001
DEFINITION PM2-AN0089-081100-011-e04 AN0089 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF734487
VERSION     BF734487.1 GI:12059724
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 165)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED    10737800
COMMENT    Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM2&t2=PM2-AN0089-
            081100-011-e04&t3=2000-11-08&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 20
            High quality sequence stop: 164.
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                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /dev_stage="Adult"
                    /clone_lib="AN0089"
                    /note="Organ: amnion normal; Vector: puc18; Site 1: SmaI;
                    Site 2: SmaI; A mini-library was made by cloning products
                    derived from ORSTES PCR (U.S. Letters Patent application
                    No. 196,716 - Ludwig Institute for Cancer Research)
                    profiles into the pUC 18 vector. Reverse transcription of
                    tissue mRNA and cDNA amplification were performed under
                    low stringency conditions."

ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
    |||||
Db 69 GGAGCTAACATCTCCAAAGTC 88

RESULT 3
LOCUS      T10413/c      222 bp      mRNA      linear      EST 29-NOV-1993
DEFINITION hbc120 Human pancreatic islet Homo sapiens cDNA clone hbc120 5'end,
            mRNA sequence.
ACCESSION  T10413
VERSION     T10413.1 GI:390567
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 222)
AUTHORS   Takeda,J., Yano,H., Eng,S., Zeng,Y. and Bell,G.I.
TITLE      A molecular inventory of human pancreatic islets: sequence analysis
            of 1000 cDNA clones
JOURNAL    Hum. Mol. Genet. 2, 1793-1798 (1993)
PUBMED    7506601
COMMENT    Contact: Bell GI or Takeda J
            HMI
            Univ. of Chicago
            5841 S. Maryland Ave., MC1028, Chicago IL 60637
            Tel: 3127029116
            Fax: 3127020271
            Email: g-bell@uchicago.edu
            Seq primer: SK primer.
            Location/Qualifiers
                1..222
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clones="hbc120"
                    /clone_lib="Human pancreatic islet"
                    /note="Vector: Lambda ZAPII; Site 1: Eco RI; Site 2: Xho
                    I; mRNA was prepared from normal adult human islets. cDNA
                    was directionally synthesized from the Xho I in the vector
                    to the EcoRI site. cDNA was size fractionated to remove
                    sequences <1000 bp in size."

ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 222;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAAGTC 20
    |||||
Db 27 GGAGCTAACATCTCCAAAGTC 8

RESULT 4
LOCUS      DY178075/c      316 bp      mRNA      linear      EST 02-FEB-2006
DEFINITION 000407BTNA005141HT BTNA Bos taurus cDNA, mRNA sequence.
ACCESSION  DY178075
VERSION     DY178075.1 GI:86382175
KEYWORDS   EST.
SOURCE     Bos taurus (cattle)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.

```

```

REFERENCE
AUTHORS 1 (bases 1 to 316)
          McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
          Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.,
          Hagemann,L., Lee,R., Hein,W., Johnstone,P., Macbool,N., McMahon,C.,
          McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J.,
          Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
          Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
          Atkinson,P.
TITLE AgResearch, Genesis and Primary Industry Victoria Bovine EST
JOURNAL project
COMMENT Unpublished (2006)
        Contact: Macbool N
        AgResearch Ltd.
        Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
        Mosgiel, New Zealand
        Email: nauman.macbool@agresearch.co.nz.

FEATURES
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        /organism="Bos taurus"
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        /tissue_type="Tonsil"
        /clone_lib="BTNA"
        /notes="Vector: pBK-CMV; Bovine tonsil cDNA library derived
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        Wayne Hein on 27/01/00"

ORIGIN
Query Match 100.0%; Score 20; DB 10; Length 316;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
   |||||
Db 277 GGAGCTAACATCTCCCAAGTC 258

RESULT 5
LOCUS CN264306/c 324 bp mRNA linear EST 16-MAY-2004
DEFINITION 1700600020922 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN264306
VERSION CN264306.1 GI:47280720
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.

REFERENCE 1 (bases 1 to 324)
          Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
          Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
          Lebkowaki,J and Stanton,L.W
          Transcriptome characterization elucidates signaling networks that
          control human ES cell growth and differentiation
          Nat. Biotechnol. 22 (6), 707-716 (2004)
          15146197
          Contact: Brandenberger R
          Regenerative Medicine
          Geron Corporation
          230 Constitution Drive, Menlo Park, CA 94025, USA
          Tel: 650 473 8658
          Fax: 650 473 7760
          Email: rbrandenberger@geron.com
          Insert Length: 324 Std Error: 0.00.
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            1..324
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              /mol_type="mRNA"
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FEATURES
source
Query Match 100.0%; Score 20; DB 7; Length 326;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
   |||||
Db 78 GGAGCTAACATCTCCCAAGTC 59

RESULT 6
LOCUS BE184816 326 bp mRNA linear EST 22-JUN-2000
DEFINITION QV4-HT0691-270400-186-g04 HT0691 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE184816
VERSION BE184816.1 GI:8664000
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.

REFERENCE 1 (bases 1 to 326)
          Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
          Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
          Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
          Brunstein,A., deoliveira,P.S., Bucher,P., Jorgeneel,C.V.,
          O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
          Simpson,A.J.
          Shotgun sequencing of the human transcriptome with ORF expressed
          sequence tags
          Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
          10737800
          Contact: Simpson A.J.G.
          Laboratory of Cancer Genetics
          Ludwig Institute for Cancer Research
          Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001
          Email: asimpson@ludwig.org.br
          This sequence was derived from the FAPESP/LICR Human Cancer Genome
          Project. This entry can be seen in the following URL
          (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=QV4-HT0691-270
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              /dev_stage="Adult"
              /clone_lib="HT0691"
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              Site 2: SmaI; A mini-library was made by cloning products
              derived from ORESTES PCR (U.S. Letters Patent application
              No. 196,716 - Ludwig Institute for Cancer Research)
              profiles into the pUC 18 vector. Reverse transcription of
              tissue mRNA and cDNA amplification were performed under
              low stringency conditions."

ORIGIN
Query Match 100.0%; Score 20; DB 7; Length 326;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCCAAGTC 20
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Db 78 GGAGCTAACATCTCCCAAGTC 59

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from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

```



McCracken, J., Stelwagen, K., Parr, V., Singh, K., Whitley, J., Nicholas, K., Savin, K., Mather, A., McPartlan, H., Whitley, J., Wells, M., Bowman, P., Goddard, M., Langford, C., McSwan, J. and Atkinson, P.

**TITLE** AgResearch, Genesis and Primary Industry Victoria Bovine EST project

**JOURNAL** Unpublished (2006)

**COMMENT** Contact: Magbool N

AgResearch Ltd.

Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,

Mosgiel, New Zealand

Email: nauman.magbool@agresearch.co.nz.

**FEATURES** Location/Qualifiers

source

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/organism="Bos taurus"

/mol\_type="mRNA"

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/tissue\_type="Liver"

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**ORIGIN**

Query Match 100.0%; Score 20; DB 10; Length 387;

Best Local Similarity 100.0%; Pred. No. 34;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1 GGAGCTAACATCTCCAAGTC 20

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**Db** 244 GGAGCTAACATCTCCAAGTC 225

**RESULT 10**

**LOCUS** D56430/c

**DEFINITION** HUM42804B Clontech human fetal brain polyA+ mRNA (#6535) Homo

sapiens cDNA clone GEN-428E04 5', mRNA sequence.

**ACCESSION** D56430

**VERSION** D56430.1 GI:971035

**KEYWORDS** EST.

**SOURCE** Homo sapiens (human)

**ORGANISM**

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 400)

Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,

Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,

Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.,

Maekawa, H., Shin, S. and Nakamura, Y.

Fujiwara et al. (1995)

**TITLE** Unpublished (1995)

**JOURNAL** Contact: Teitomu Fujiwara

Otsuka GEN Research Institute

Otsuka Pharmaceutical Co., Ltd

463-10 kagauno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan

Tel: 0886-65-2888

Fax: 0886-37-1035.

**FEATURES** Location/Qualifiers

source

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="GEN-428E04"

/clone\_lib="Clontech human fetal brain polyA+ mRNA

(#6535)"

**ORIGIN**

Query Match

Best Local Similarity 100.0%; Score 20; DB 9; Length 400;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1 GGAGCTAACATCTCCAAGTC 20

|||||

**Db** 193 GGAGCTAACATCTCCAAGTC 174

**RESULT 11**

**LOCUS** AW800395/c

**DEFINITION** MR2-UM0061-050400-105-a08

**ACCESSION** AW800395

**VERSION** AW800395.1

**KEYWORDS** GI:7852265

**SOURCE** EST.

**ORGANISM** Homo sapiens (human)

**REFERENCE** 1 (bases 1 to 421)

**AUTHORS** Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.P., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

10737800

**COMMENT** Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the PAFESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=MR2-UM0061-050

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**Location/Qualifiers**

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/organism="Homo sapiens"

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/dev\_stage="Adult"

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SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No.

196,716 - Ludwig Institute for Cancer Research) profiles

into the puc 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

**ORIGIN**

Query Match

Best Local Similarity 100.0%; Score 20; DB 7; Length 421;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1 GGAGCTAACATCTCCAAGTC 20

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**Db** 278 GGAGCTAACATCTCCAAGTC 259

**RESULT 12**

**LOCUS** BE696421

**DEFINITION** QVO-C70383-300600-290-h02 CT0383 Homo sapiens cDNA, mRNA sequence.

**ACCESSION** BE696421



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VERSION      BE696412.1  GI:10083581
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 421)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
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              High quality sequence stop: 421.
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                  /clone_lib="CT0383"
                  /note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:
                  SmaI; A mini-library was made by cloning products derived
                  from ORESTES PCR (U.S. Letters Patent application No.
                  196,716 - Ludwig Institute for Cancer Research) profiles
                  into the pUC 18 vector. Reverse transcription of tissue
                  mRNA and cDNA amplification were performed under low
                  stringency conditions."

ORIGIN
Query Match      100.0%; Score 20; DB 7; Length 421;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 18 GGAGCTACATCTCCAGTC 37

RESULT 13
LOCUS      DY048267/c
DEFINITION DY048267
ACCESSION DY048267
VERSION    DY048267.1  GI:86187810
KEYWORDS   EST.
SOURCE     Bos taurus (cattle)
ORGANISM   Bos taurus
REFERENCE  1 (bases 1 to 424)
AUTHORS    McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
              Glenn,M., Havukala,I., Watson,J., Crawford,A., Wheeler,T.,
              Hagemann,L., Lee,R., Hein,W., Johnstone,P., Magbool,N., McMahon,C.,
              McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J.,
              Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
              Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
              Atkinson,P.
              AgResearch, Genesis and Primary Industry Victoria Bovine EST
              Project
              Unpublished (2006)
              Contact: Magbool N
              AgResearch Ltd.
              Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
              Mosgiel, New Zealand
              Email: nauman.magbool@agresearch.co.nz.
              Location/Qualifiers
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                  /tissue_type="Liver"
                  /clone_lib="BLIB"
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                  derived from tissue harvested from an unknown breed calf
                  by Allan Crawford on 28/09/99"

ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 424;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTACATCTCCAGTC 20
    |||||
DB 244 GGAGCTACATCTCCAGTC 225

RESULT 14
LOCUS      BE696412
DEFINITION QV0-CT0383-300600-290-e05 CT0383 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BE696412
VERSION     BE696412.1  GI:10083572
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    1 (bases 1 to 445)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
              Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=42&t=QV0-CT0383-300)
              600-290-e05&t3=2000-06-30&t4=1
              Seq primer: puc 18 forward
              High quality sequence start: 29
              High quality sequence stop: 445.
              Location/Qualifiers

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1. .445
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0383"
/notes="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORSTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN
Query Match 100.0%; Score 20; DB 7; Length 445;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
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Db 33 GGAGCTAACATCTCCAAGTC 52

RESULT 15
AQ805950/c
LOCUS
DEFINITION
HS_3025_A2_C03_MR_CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plates=3025 Col=6 Row=E, genomic survey
sequence.
ACCESSION
AQ805950
VERSION
AQ805950.1 GI:5723212
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 453)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3025 row: E column: 6
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 453.
FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=3025 Col=6 Row=E"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/notes="Organ: sperm; Vector: pBelOBAC11; BAC Clones in
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ORIGIN
Query Match 100.0%; Score 20; DB 11; Length 453;
Best Local Similarity 100.0%; Pred. No. 35;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
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Db 225 GGAGCTAACATCTCCAAGTC 206

Search completed: May 21, 2006, 22:31:08
Job time : 2226.5 secs
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RESULT 2  
US-09-949-016-1518/c  
Sequence 1518, Application US/09949016  
Patent No. 6812339  
General Information:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN  
WITH HUMAN DISEASE  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ IDS: 207012

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1518
; LENGTH: 2770
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1518

Query Match      100.0%; Score 20; DB 3; Length 2770;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
Db 811 GGAGCTAACATCTCCAAGTC 792

RESULT 3
US-09-919-039-148/c
; Sequence 148, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 148
; LENGTH: 3229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 1250434CB1
US-09-919-039-148

Query Match      100.0%; Score 20; DB 3; Length 3229;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
Db 1958 GGAGCTAACATCTCCAAGTC 1939

RESULT 4
US-09-380-662-22/c
; Sequence 22, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22
; LENGTH: 3678
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(2509)

US-09-380-662-22

Query Match      100.0%; Score 20; DB 3; Length 3678;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
Db 1719 GGAGCTAACATCTCCAAGTC 1700

RESULT 5
US-09-959-873B-19/c
; Sequence 19, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 3678
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-959-873B-19

Query Match      100.0%; Score 20; DB 3; Length 3678;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
Db 1719 GGAGCTAACATCTCCAAGTC 1700

RESULT 6
US-10-028-158-22/c
; Sequence 22, Application US/10028158
; Patent No. 6863880
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
; TITLE OF INVENTION: TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/10/028,158
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/09/380,662
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22
; LENGTH: 3678
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (29)..(2509)
US-10-028-158-22

Query Match      100.0%; Score 20; DB 3; Length 3678;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
Db 1719 GGAGCTAACATCTCCAAGTC 1700

RESULT 7
US-08-480-473B-1/c
; Sequence 1, Application US/08480473B
; Patent No. 5882914
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3736 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-480-473B-1

Query Match      100.0%; Score 20; DB 2; Length 3736;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
Db 1719 GGAGCTAACATCTCCAAGTC 1700

RESULT 8
US-08-915-213-1/c
; Sequence 1, Application US/08915213
; Patent No. 6020462
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
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; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,213
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3736 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-915-213-1

Query Match      100.0%; Score 20; DB 3; Length 3736;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
Db 1719 GGAGCTAACATCTCCAAGTC 1700

RESULT 9
US-09-148-547-1/c
; Sequence 1, Application US/09148547
; Patent No. 6124131
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: Hypoxia Inducible Factor-1 and Methods of Use
; FILE REFERENCE: 07265/151001
; CURRENT APPLICATION NUMBER: US/09/148,547
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3736
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(2509)
US-09-148-547-1

Query Match      100.0%; Score 20; DB 3; Length 3736;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20
Db 1719 GGAGCTAACATCTCCAAGTC 1700

RESULT 10
US-09-235-217-1/c
; Sequence 1, Application US/09235217
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Patent No. 6222018  
; GENERAL INFORMATION:  
; APPLICANT: Semenza, Gregg L.  
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/235,217  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/480,473  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07265/053001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-09-235-581-1

Query Match 100.0%; Score 20; DB 3; Length 3736;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20  
DB 1719 GGAGCTAACATCTCCAAGTC 1700

RESULT 11  
US-09-383-581-1/c  
; Sequence 1, Application US/09383581  
; Patent No. 6562799  
; GENERAL INFORMATION:  
; APPLICANT: Semenza, Gregg L.  
; TITLE OF INVENTION: STABLE HYPOXIA INDUCIBLE FACTOR-1 alpha  
; TITLE OF INVENTION: AND METHOD OF USE  
; FILE REFERENCE: JHU1500-1  
; CURRENT APPLICATION NUMBER: US/09/383,581  
; CURRENT FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: 09/148,547  
; PRIOR FILING DATE: 1998-08-25  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3736  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29) ... (2509)  
US-09-383-581-1

Query Match 100.0%; Score 20; DB 3; Length 3736;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20  
DB 1719 GGAGCTAACATCTCCAAGTC 1700

RESULT 12  
PCT-US96-10251-1/c  
; Sequence 1, Application PC/TUS9610251  
; GENERAL INFORMATION:  
; APPLICANT: The Johns Hopkins University School of Medicine  
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/10251  
; FILING DATE: 06-JUN-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07265/053W01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3736 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
PCT-US96-10251-1

Query Match 100.0%; Score 20; DB 7; Length 3736;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20  
DB 1719 GGAGCTAACATCTCCAAGTC 1700

RESULT 13  
US-09-949-016-218/c  
; Sequence 218, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 218  
; LENGTH: 3933  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-218

Query Match 100.0%; Score 20; DB 3; Length 3933;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20  
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Db 1955 GGAGCTAACATCTCCAAGTC 1936

RESULT 14  
US-09-949-016-13260/c  
; Sequence 13260, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13260  
; LENGTH: 18120  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13260

Query Match 100.0%; Score 20; DB 3; Length 18120;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20  
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Db 8653 GGAGCTAACATCTCCAAGTC 8634

RESULT 15  
US-09-949-016-11960/c  
; Sequence 11960, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11960  
; LENGTH: 56714

; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-11960

Query Match 100.0%; Score 20; DB 3; Length 56714;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 47248 GGAGCTAACATCTCCAAGTC 47229

Search completed: May 21, 2006, 21:20:58  
Job time : 82.5 secs

GenCore version 5.1.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: May 21, 2006, 21:21:21 ; Search time 823 Seconds  
(without alignments)  
298.606 Million cell updates/sec  
Title: US-10-766-185-4  
Perfect score: 20  
Sequence: 1 ggagctaacatctccaagtc 20  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 1892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10H\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10I\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10J\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10K\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
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C 2	20	100.0	20	8	US-10-766-185-4
C 3	20	100.0	60	3	US-09-908-975-6413
C 4	20	100.0	2481	3	US-09-922-958-3
C 5	20	100.0	2481	8	US-10-384-339C-38
C 6	20	100.0	2487	10	US-10-450-763-20859
C 7	20	100.0	2517	3	US-09-967-388-3
C 8	20	100.0	2528	7	US-10-204-724-2
C 9	20	100.0	2861	7	US-10-264-049-431
C 10	20	100.0	3180	7	US-10-425-784-3
C 11	20	100.0	3229	3	US-09-919-039-148
C 12	20	100.0	3229	6	US-10-208-408-22
C 13	20	100.0	3229	7	US-10-084-817-113
C 14	20	100.0	3229	6	US-10-247-671-19
C 15	20	100.0	3551	8	US-10-304-126-13
C 16	20	100.0	3551	9	US-10-719-370A-13
C 17	20	100.0	3678	6	US-10-028-158-22

C 18	20	100.0	3678	9	US-10-901-583-19
C 19	20	100.0	3678	10	US-10-007-255-3
C 20	20	100.0	3678	13	US-11-043-493-22
C 21	20	100.0	3736	7	US-10-423-419-1
C 22	20	100.0	3736	10	US-10-831-380-1
C 23	20	100.0	3812	9	US-10-699-557-3
C 24	20	100.0	3927	3	US-09-833-790-231
C 25	20	100.0	3933	7	US-10-172-118-625
C 26	20	100.0	3933	7	US-10-388-360-309
C 27	20	100.0	3933	8	US-10-342-887-625
C 28	20	100.0	3933	8	US-10-407-807-1
C 29	20	100.0	3933	8	US-10-304-126-4
C 30	20	100.0	3933	9	US-10-719-370A-4
C 31	20	100.0	3933	9	US-10-719-370A-133
C 32	20	100.0	3933	9	US-10-848-646-3
C 33	20	100.0	3933	10	US-10-956-157-643
C 34	20	100.0	3933	10	US-10-494-800-59
C 35	20	100.0	3933	16	US-11-288-720-1
C 36	20	100.0	3958	9	US-10-699-557-2
C 37	20	100.0	4162	10	US-10-450-763-20862
C 38	20	100.0	4656	6	US-10-044-090-284
C 39	20	100.0	4727	7	US-10-115-987B-12
C 40	20	100.0	4740	7	US-10-115-987B-13
C 41	20	100.0	10355	7	US-10-204-724-4
C 42	20	100.0	57500	9	US-10-719-370A-11
C 43	20	100.0	57501	8	US-10-304-126-11
C 44	18.4	92.0	2481	6	US-10-101-816-1
C 45	18.4	92.0	2481	9	US-10-854-483-1

ALIGNMENTS

RESULT 1  
US-10-766-185-3/c  
; Sequence 3, Application US/10766185  
; Publication No. US20040152655A1  
; GENERAL INFORMATION:  
; APPLICANT: Yoon, Heejeong  
; APPLICANT: Ahn, Chang Ho  
; APPLICANT: Lee, Young Bok  
; APPLICANT: Mao, Lingjun  
; APPLICANT: Jiang, Xiaoming  
; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1  
; FILE REFERENCE: REX 7034  
; CURRENT APPLICATION NUMBER: US/10766,185  
; CURRENT FILING DATE: 2004-01-28  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: human  
US-10-766-185-3

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGAGCTAACATCTCCAAATC 20  
Db 20 GGAGCTAACATCTCCAAATC 1

RESULT 2  
US-10-766-185-4  
; Sequence 4, Application US/10766185  
; Publication No. US20040152655A1  
; GENERAL INFORMATION:  
; APPLICANT: Yoon, Heejeong  
; APPLICANT: Ahn, Chang Ho  
; APPLICANT: Lee, Young Bok  
; APPLICANT: Mao, Lingjun



Mon May 22 14:33:54 2006

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; APPLICANT: Jiang, Xiaoming
; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
; FILE REFERENCE: REX 7034
; CURRENT APPLICATION NUMBER: US/10/766.185
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense oligonucleotide
US-10-766-185-4

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Best Local Similarity 100.0%; Pred. No. 4.4; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
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Db 1 GGAGCTAACATCTCCAAGTC 20

RESULT 3
US-09-908-975-6413/c
; Sequence 6413, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6413
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-6413

Query Match      100.0%; Score 20; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.9; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
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Db 51 GGAGCTAACATCTCCAAGTC 32

RESULT 4
US-09-922-958-3/c
; Sequence 3, Application US/09922958
; Patent No. US20020048794A1
; GENERAL INFORMATION:
; APPLICANT: POELLINGER, Lorenz
; APPLICANT: PEREIRA, Teresa
; APPLICANT: RUAS, Jorge
; TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACTOR-1
; TITLE OF INVENTION: THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN
; FILE REFERENCE: 3743/49008
; CURRENT APPLICATION NUMBER: US/09/922,958
; CURRENT FILING DATE: 2001-08-07
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; PRIOR APPLICATION NUMBER: US 60/223,480
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2481
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2478)
US-09-922-958-3

Query Match      100.0%; Score 20; DB 3; Length 2481;
Best Local Similarity 100.0%; Pred. No. 7.3; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
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Db 1691 GGAGCTAACATCTCCAAGTC 1672

RESULT 5
US-10-384-339C-38/c
; Sequence 38, Application US/10384339C
; Publication No. US20040175703A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Roland
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET
; FILE REFERENCE: 20200/2002
; CURRENT APPLICATION NUMBER: US/10/384,339C
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: DE 10155280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 10158411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 10160151.4
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 2481
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: HIF-alpha
; PATENT DOCUMENT NUMBER: U22431
US-10-384-339C-38

Query Match      100.0%; Score 20; DB 8; Length 2481;
Best Local Similarity 100.0%; Pred. No. 7.3; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
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Db 1691 GGAGCTAACATCTCCAAGTC 1672

RESULT 6
US-10-450-763-20859/c
; Sequence 20859, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
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; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 20859
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (574)..(2487)
; OTHER INFORMATION: 9% homologous to Homo sapiens 06-JUN-1995 Human hypoxia
; OTHER INFORMATION: Inducible factor-1 alpha cDNA, accession number T45937_cdl, Smith-
US-10-450-763-20859

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Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 2487;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
Db 1697 GGAGCTAACATCTCCAAAGTC 1678

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RESULT 7
US-09-967-388-3/c
; Sequence 3, Application US/09967388
; Publication No. US20030103956A1
; GENERAL INFORMATION:
; APPLICANT: JEFFEREY M. ARBEIT
; TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
; FILE REFERENCE: UC077_001A
; CURRENT APPLICATION NUMBER: US/09/967,388
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2517
; TYPE: DNA
; ORGANISM: HUMAN
US-09-967-388-3

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Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 2517;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
Db 1727 GGAGCTAACATCTCCAAAGTC 1708

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RESULT 8
US-10-764-724-2/c
; Sequence 2, Application US/10204724
; Publication No. US20030180740A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, John Alan
; TITLE OF INVENTION: DIFFERENTIAL EXPRESSION SCREENING METHOD
; FILE REFERENCE: 53262000200
; CURRENT APPLICATION NUMBER: US/10/204,724
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: PCT/GB01/00758
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: GB 0018679.1
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: GB 0004197.0
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 16

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2528
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-204-724-2

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Query Match
Best Local Similarity 100.0%; Score 20; DB 7; Length 2528;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
Db 1718 GGAGCTAACATCTCCAAAGTC 1699

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RESULT 9
US-10-264-049-431/c
; Sequence 431, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 431
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2853)..(2853)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-431

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Query Match
Best Local Similarity 100.0%; Score 20; DB 7; Length 2861;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
Db 841 GGAGCTAACATCTCCAAAGTC 822

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RESULT 10
US-10-425-784-3/c
; Sequence 3, Application US/10425784
; Publication No. US20040009591A1
; GENERAL INFORMATION:
; APPLICANT: Comer, Allen
; APPLICANT: Hoffmann, Michael
; APPLICANT: Allen-Hoffmann, Lynn
; TITLE OF INVENTION: Keratinocytes Expressing Exogenous Angiogenic Growth Factors
; FILE REFERENCE: STRATA-08110
; CURRENT APPLICATION NUMBER: US/10/425,784
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 60/376,488
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 3180
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-425-784-3

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Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1955 GGAGCTAACATCTCCAAGTC 1936

RESULT 11  
US-09-919-039-148/c  
; Sequence 148, Application US/09919039  
; Publication No. US20030108871A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES  
; FILE REFERENCE: PA-0035 US  
; CURRENT APPLICATION NUMBER: US/09/919,039  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 60/222,113  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 401  
; SOFTWARE: PERL Program  
; SEQ ID NO 148  
; LENGTH: 3229  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1250434CB1  
US-09-919-039-148

Query Match 100.0%; Score 20; DB 3; Length 3229;  
Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20  
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DB 1958 GGAGCTAACATCTCCAAGTC 1939

RESULT 12  
US-10-208-408-22/c  
; Sequence 22, Application US/10208408  
; Publication No. US20030096272A1  
; GENERAL INFORMATION:  
; APPLICANT: Schebye, Xiao Min  
; TITLE OF INVENTION: GENES REGULATED BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR  
; FILE REFERENCE: PA-0048-1 US  
; CURRENT APPLICATION NUMBER: US/10/208,408  
; CURRENT FILING DATE: 2002-07-29  
; PRIOR APPLICATION NUMBER: 60/308,868  
; PRIOR FILING DATE: 2001-07-30  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PERL Program  
; SEQ ID NO 22  
; LENGTH: 3229  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030096272A1 1250434CB1  
US-10-208-408-22

Query Match 100.0%; Score 20; DB 6; Length 3229;  
Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20  
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DB 1958 GGAGCTAACATCTCCAAGTC 1939

RESULT 13  
US-10-084-817-113/c  
; Sequence 113, Application US/10084817  
; Publication No. US20030119009A1  
; GENERAL INFORMATION:  
; APPLICANT: Susan Stuart  
; APPLICANT: Jed G. Nuchtern  
; APPLICANT: Sharon E. Pion  
; APPLICANT: Jason M. Shohet  
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION  
; FILE REFERENCE: PA-0046 US  
; CURRENT APPLICATION NUMBER: US/10/084,817  
; CURRENT FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/270,784  
; PRIOR FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 365  
; SOFTWARE: PERL Program  
; SEQ ID NO 113  
; LENGTH: 3229  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030119009A1 1250434CB1  
US-10-084-817-113

Query Match 100.0%; Score 20; DB 6; Length 3229;  
Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGTC 20  
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DB 1958 GGAGCTAACATCTCCAAGTC 1939

RESULT 14  
US-10-247-671-19/c  
; Sequence 19, Application US/10247671  
; Publication No. US20030194721A1  
; GENERAL INFORMATION:  
; APPLICANT: Mikita, Thomas  
; APPLICANT: Shiffman, Dov  
; APPLICANT: Porter, Gordon, J.  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS  
; FILE REFERENCE: PA-0050 US  
; CURRENT APPLICATION NUMBER: US/10/247,671  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: 60/323,784  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 186  
; SOFTWARE: PERL Program  
; SEQ ID NO 19  
; LENGTH: 3229  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1250434CB1  
US-10-247-671-19

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Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1958 GGAGCTAACATCTCCAAGTC 1939

RESULT 15  
US-10-304-126-13/c  
; Sequence 13, Application US/10304126

; Publication No. US20040101858A1  
; GENERAL INFORMATION:  
; APPLICANT: Donna T. Ward  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: MODULATION OF HYPOXIA-INDUCIBLE FACTOR 1 ALPHA EXPRESSION  
; FILE REFERENCE: PTS-0070  
; CURRENT APPLICATION NUMBER: US/10/304,126  
; CURRENT FILING DATE: 2002-11-23  
; NUMBER OF SEQ ID NOS: 132  
; SEQ ID NO 13  
; LENGTH: 3551  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29)...(2236)  
US-10-304-126-13

Query Match 100.0%; Score 20; DB 8; Length 3551;  
Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1719 GGAGCTAACATCTCCAGTC 1700

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Job time : 824 secs

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:33:45 ; Search time 13.5 seconds  
(without alignments)  
104.527 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggaagtaacatctccaagtc 20

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Searched: 224314 seqs, 35277956 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.4	77.0	25	7	US-11-217-529-23140
2	15.4	77.0	1080	7	US-11-217-529-1559
3	15.2	76.0	25	7	US-11-217-529-107428
4	15.2	76.0	590	6	US-10-488-619-2776
5	15.2	76.0	630	7	US-11-217-529-3916
6	15.2	76.0	1080	7	US-11-217-529-77549
7	14.8	74.0	2823	7	US-11-217-529-4032
8	14.8	74.0	6075	7	US-11-217-529-3047
9	14.4	72.0	2397	7	US-11-217-529-254
10	14.2	71.0	432	7	US-11-217-529-2519
11	14.2	71.0	537	7	US-11-301-554-1175
12	14.2	71.0	1710	7	US-11-024-544A-58
13	14.2	71.0	1710	7	US-11-190-750-35
14	14.2	71.0	5105	7	US-11-024-544A-82
15	14.2	71.0	5105	7	US-11-190-750-63
16	14.2	71.0	5105	7	US-11-264-784-157
17	14.2	71.0	6457	7	US-11-264-784-117
18	14.2	71.0	7145	7	US-11-264-784-121
19	14.2	71.0	7323	7	US-11-024-544A-168
20	14.2	71.0	7323	7	US-11-024-545-68
21	14.2	71.0	7323	7	US-11-251-466-53
22	14.2	71.0	7323	7	US-11-254-173-61
23	14.2	71.0	7323	7	US-11-264-784-140
24	14.2	71.0	7822	7	US-11-024-544A-144
25	14.2	71.0	7822	7	US-11-264-784-153

c 26	14.2	71.0	7879	7	US-11-264-784-119	Sequence 119, App
c 27	14.2	71.0	7930	7	US-11-264-784-154	Sequence 154, App
c 28	14.2	71.0	8015	7	US-11-251-466-41	Sequence 41, Appl
c 29	14.2	71.0	8015	7	US-11-264-784-138	Sequence 138, App
c 30	14.2	71.0	8084	7	US-11-024-545-67	Sequence 67, Appl
c 31	14.2	71.0	8084	7	US-11-264-784-142	Sequence 142, App
c 32	14.2	71.0	8165	7	US-11-024-544A-164	Sequence 164, App
c 33	14.2	71.0	8165	7	US-11-024-545-64	Sequence 64, Appl
c 34	14.2	71.0	8165	7	US-11-251-466-40	Sequence 40, Appl
c 35	14.2	71.0	8165	7	US-11-254-173-65	Sequence 65, Appl
c 36	14.2	71.0	8165	7	US-11-264-784-118	Sequence 118, App
c 37	14.2	71.0	8179	7	US-11-264-784-155	Sequence 155, App
c 38	14.2	71.0	8194	7	US-11-024-544A-128	Sequence 128, App
c 39	14.2	71.0	8194	7	US-11-024-545-56	Sequence 56, Appl
c 40	14.2	71.0	8194	7	US-11-190-750-111	Sequence 111, App
c 41	14.2	71.0	8194	7	US-11-251-466-30	Sequence 30, Appl
c 42	14.2	71.0	8194	7	US-11-264-784-129	Sequence 129, App
c 43	14.2	71.0	8273	7	US-11-264-784-152	Sequence 152, App
c 44	14.2	71.0	8411	7	US-11-251-466-52	Sequence 52, Appl
c 45	14.2	71.0	8411	7	US-11-264-784-139	Sequence 139, App

#### ALIGNMENTS

RESULT 1

US-11-217-529-23140

; Sequence 23140, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 23140

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

; US-11-217-529-23140

Query Match 77.0%; Score 15.4; DB 7; Length 25;

Best Local Similarity 94.1%; Pred. No. 6;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCTAACATCTCCAAGTC 20

|||||

Db 5 GCTAAGATCTCCAAGTC 21

RESULT 2

US-11-217-529-1559

; Sequence 1559, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529

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; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1559
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1559

Query Match      77.0%; Score 15.4; DB 7; Length 1080;
Best Local Similarity 94.1%; Pred. No. 12;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 GCTAACATCTCCAAGTC 20
Db      1030 GCTAAGATCTCCAAGTC 1046

RESULT 3
US-11-217-529-107428
; Sequence 107428, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 107428
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-107428

Query Match      76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 7.7;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGAGCTAACATCTCCAAGTC 20
Db      5 GGTGCTAAGATCACCAGTC 24

RESULT 4
US-10-488-619-2776/c
; Sequence 2776, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2776
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2776
```

```
Query Match      76.0%; Score 15.2; DB 6; Length 590;
Best Local Similarity 85.0%; Pred. No. 13;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGAGCTAACATCTCCAAGTC 20
Db      539 GGAGATGACATGTCCAAGTC 520

RESULT 5
US-11-217-529-3916
; Sequence 3916, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3916
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3916

Query Match      76.0%; Score 15.2; DB 7; Length 630;
Best Local Similarity 85.0%; Pred. No. 13;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGAGCTAACATCTCCAAGTC 20
Db      61 GAAGCTAATATCACCAGTC 80

RESULT 6
US-11-217-529-77549
; Sequence 77549, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77549
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77549

Query Match      76.0%; Score 15.2; DB 7; Length 1080;
Best Local Similarity 85.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGAGCTAACATCTCCAAGTC 20
```

Db 1027 GGTGCTAAGATCACCAGTC 1046  
|| ||||| ||| |||||

## RESULT 7

US-11-217-529-4032  
; Sequence 4032, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4032  
; LENGTH: 2823  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-4032

Query Match 74.0%; Score 14.8; DB 7; Length 2823;  
Best Local Similarity 88.9%; Pred. No. 28;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAG 18  
||| ||||| ||||| |||||  
Db 192 GGAATTAACATCTCCAAG 209

## RESULT 8

US-11-217-529-3047  
; Sequence 3047, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3047  
; LENGTH: 6075  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-3047

Query Match 74.0%; Score 14.8; DB 7; Length 6075;  
Best Local Similarity 88.9%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAAGT 19  
||| ||||| ||||| |||||  
Db 3391 GAGCTAACATCTCAAT 3408

## RESULT 9

US-11-217-529-254  
; Sequence 254, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 254  
; LENGTH: 2397  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-254

Query Match 72.0%; Score 14.4; DB 7; Length 2397;  
Best Local Similarity 93.8%; Pred. No. 44;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGCTAACATCTCCAAG 18  
| ||||| ||||| |||||  
Db 581 ATCTAACATCTCCAAG 596

## RESULT 10

US-11-217-529-2519  
; Sequence 2519, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2519  
; LENGTH: 432  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-2519

Query Match 71.0%; Score 14.2; DB 7; Length 432;  
Best Local Similarity 84.2%; Pred. No. 41;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAAGT 19  
| ||||| ||||| |||||  
Db 202 GAAGCTAACATCTCAAGT 220

## RESULT 11

US-11-301-554-1175/c  
; Sequence 1175, Application US/11301554  
; Publication No. US20060088527A1  
; GENERAL INFORMATION:  
; APPLICANT: Henderson, Robert A.

```
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; PRIOR FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1175
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-1175

Query Match 71.0%; Score 14.2; DB 7; Length 537;
Best Local Similarity 84.2%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGCTAACATCTCCAACT 19
Db 499 GGAGCTGACTTCGCCAAGT 481

RESULT 12
US-11-024-544A-58
; Sequence 58, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-1175
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; TYPE: DNA
; ORGANISM: Yarrowia lipolytica
US-11-024-544A-58

Query Match 71.0%; Score 14.2; DB 7; Length 1710;
Best Local Similarity 84.2%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAAAGTC 20
Db 404 GAGCTAACGTCACAAAGTC 422

RESULT 13
US-11-190-750-35
; Sequence 35, Application US/11190750
; Publication No. US20060094088A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Yadav, Narendra
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: ACYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF
; FILE REFERENCE: CL2718
; CURRENT APPLICATION NUMBER: US/11/190,750
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Yarrowia lipolytica
US-11-190-750-35

Query Match 71.0%; Score 14.2; DB 7; Length 1710;
Best Local Similarity 84.2%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCTAACATCTCCAAAGTC 20
Db 404 GAGCTAACGTCACAAAGTC 422

RESULT 14
US-11-024-544A-82/c
; Sequence 82, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82
; LENGTH: 5105
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid plv13
; NAME/KEY: misc feature
; LOCATION: (4446)..(4446)
; OTHER INFORMATION: n is a, c, g, or t
US-11-024-544A-82
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Query Match 71.0%; Score 14.2; DB 7; Length 5105;  
 Best Local Similarity 84.2%; Pred. No. 63;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GAGCTAACATCTCCAAAGTC 20  
 |||||  
 Db 3692 GAGCTAACGTCCACAAAGTC 3674

RESULT 15  
 US-11-190-750-63/c  
 ; Sequence 63, Application US/11190750  
 ; Publication No. US20060094089A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: E.I. duPont de Nemours and Company, Inc.  
 ; APPLICANT: Picataggio, Stephen K.  
 ; APPLICANT: Yadav, Narendra  
 ; APPLICANT: Zhang, Hongxiang  
 ; TITLE OF INVENTION: ACYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF  
 ; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF  
 ; TITLE OF INVENTION: OLEAGINOUS ORGANISMS  
 ; FILE REFERENCE: CL2718  
 ; CURRENT APPLICATION NUMBER: US/11/190,750  
 ; CURRENT FILING DATE: 2005-07-27  
 ; NUMBER OF SEQ ID NOS: 159  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 63  
 ; LENGTH: 5105  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Plasmid pLV13  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (4446)..(4446)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 US-11-190-750-63

Query Match 71.0%; Score 14.2; DB 7; Length 5105;  
 Best Local Similarity 84.2%; Pred. No. 63;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GAGCTAACATCTCCAAAGTC 20  
 |||||  
 Db 3692 GAGCTAACGTCCACAAAGTC 3674

Search completed: May 21, 2006, 21:34:20  
 Job time : 14.5 secs

STIC-Biotech/ChemLib

190173

From: McGarry, Sean  
Sent: Tuesday, May 16, 2006 12:44 PM  
To: STIC-Biotech/ChemLib  
Subject: SEQ SEARCH 10/766185

Sean McGarry 73484  
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571.272.0761  
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10/766,185

Please, a length limited search of SEQ ID NOS: 2 and (4 nt ≤ 50).

Please also a standard search of SEQ ID NOS: 2 and 4.

Thank You

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Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search NA# \_\_\_\_\_  
AA# \_\_\_\_\_  
S/L: \_\_\_\_\_  
Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_  
Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_  
Litigation: \_\_\_\_\_

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Vendors and cost where applicable STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_